Figure 1. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 8 recurrent versus 13 non-recurrent human prostate tumors for 19 genes of the concordant class

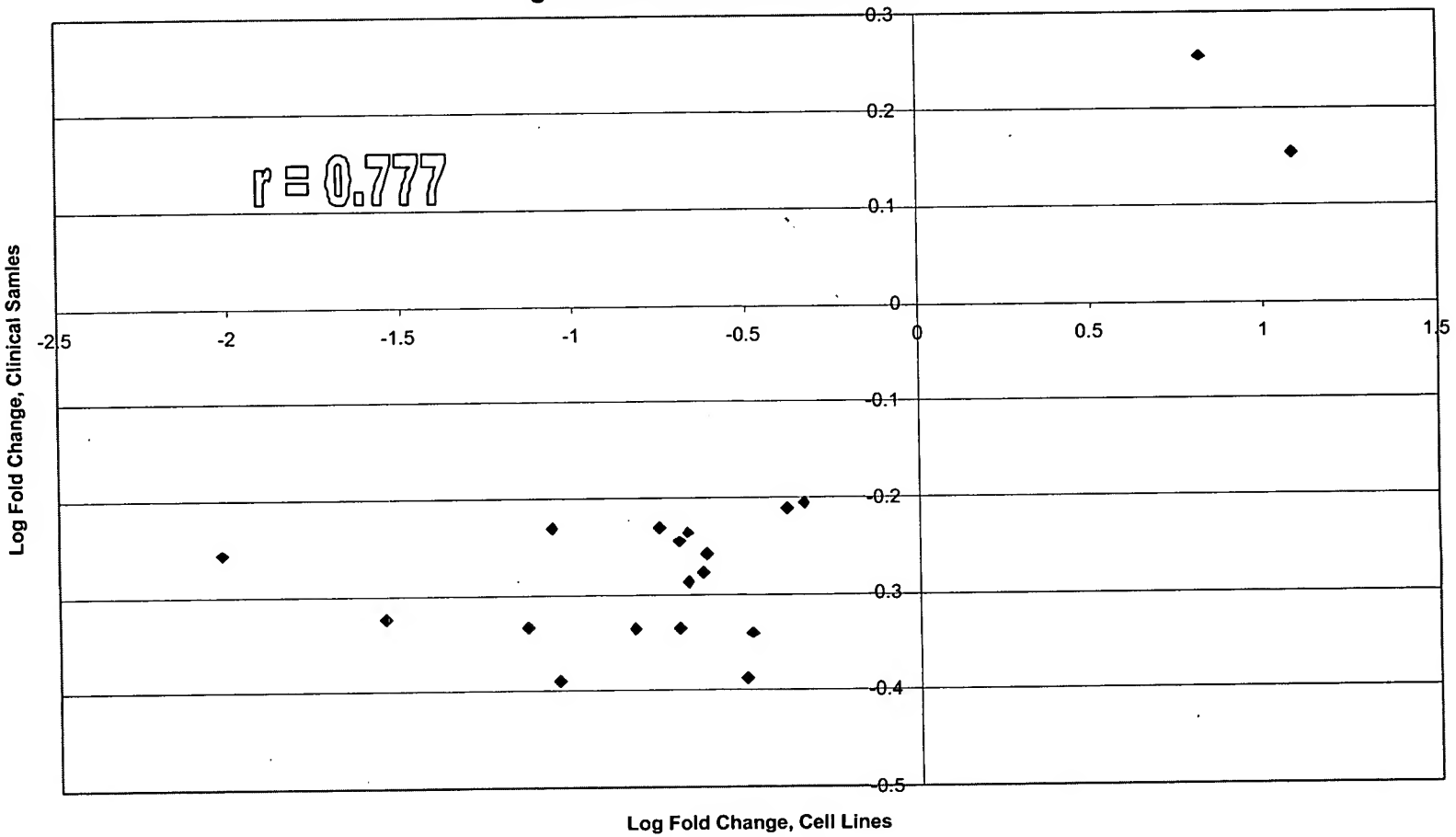


Figure 2. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 8 recurrent versus 13 non-recurrent human prostate tumors for 9 genes of the PC3/LNCap consensus class (recurence predictor class)

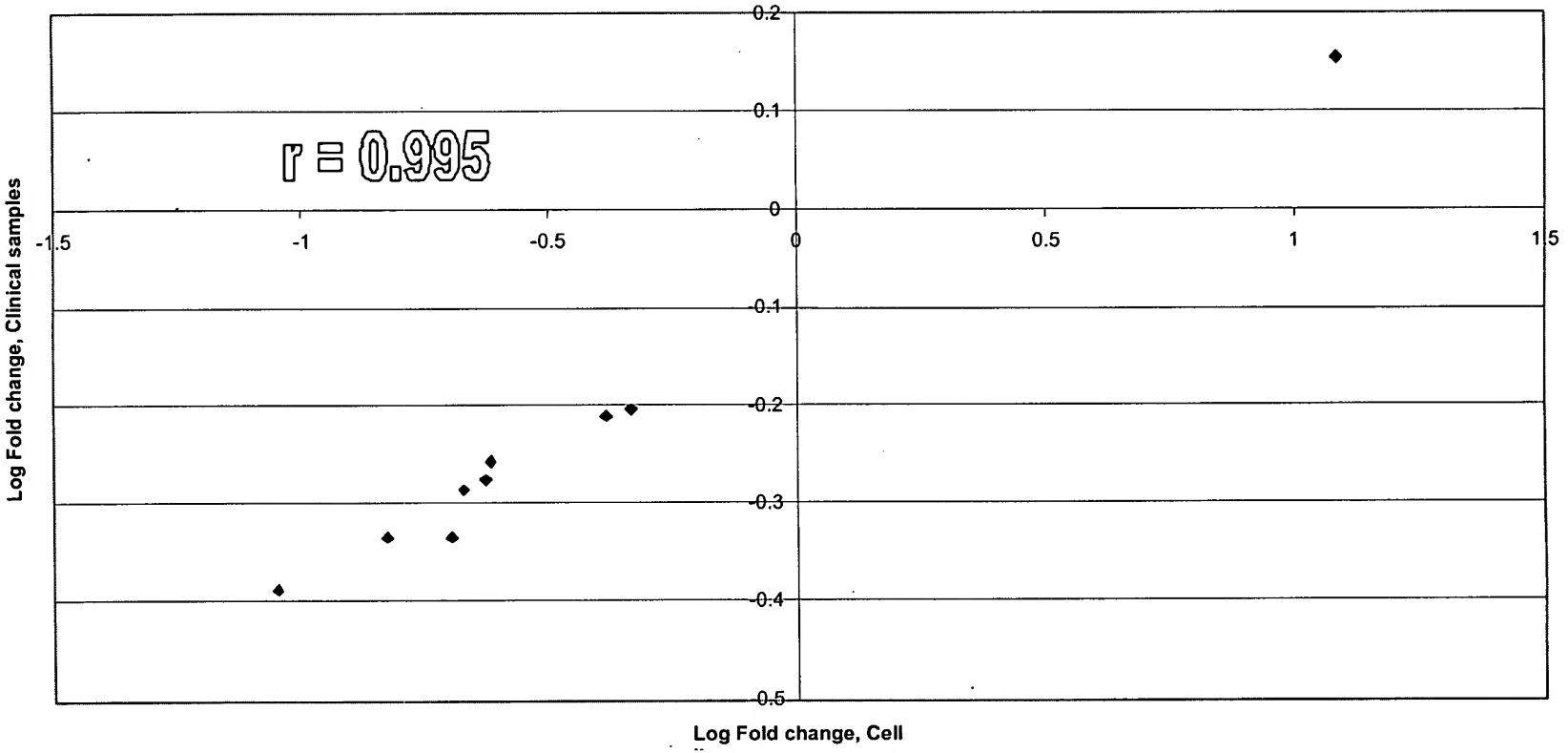


Figure 3. Association indexes for 9 genes of the recurrence predictor class in individual human prostate tumors exhibiting recurrent or non-recurrent clinical behavior

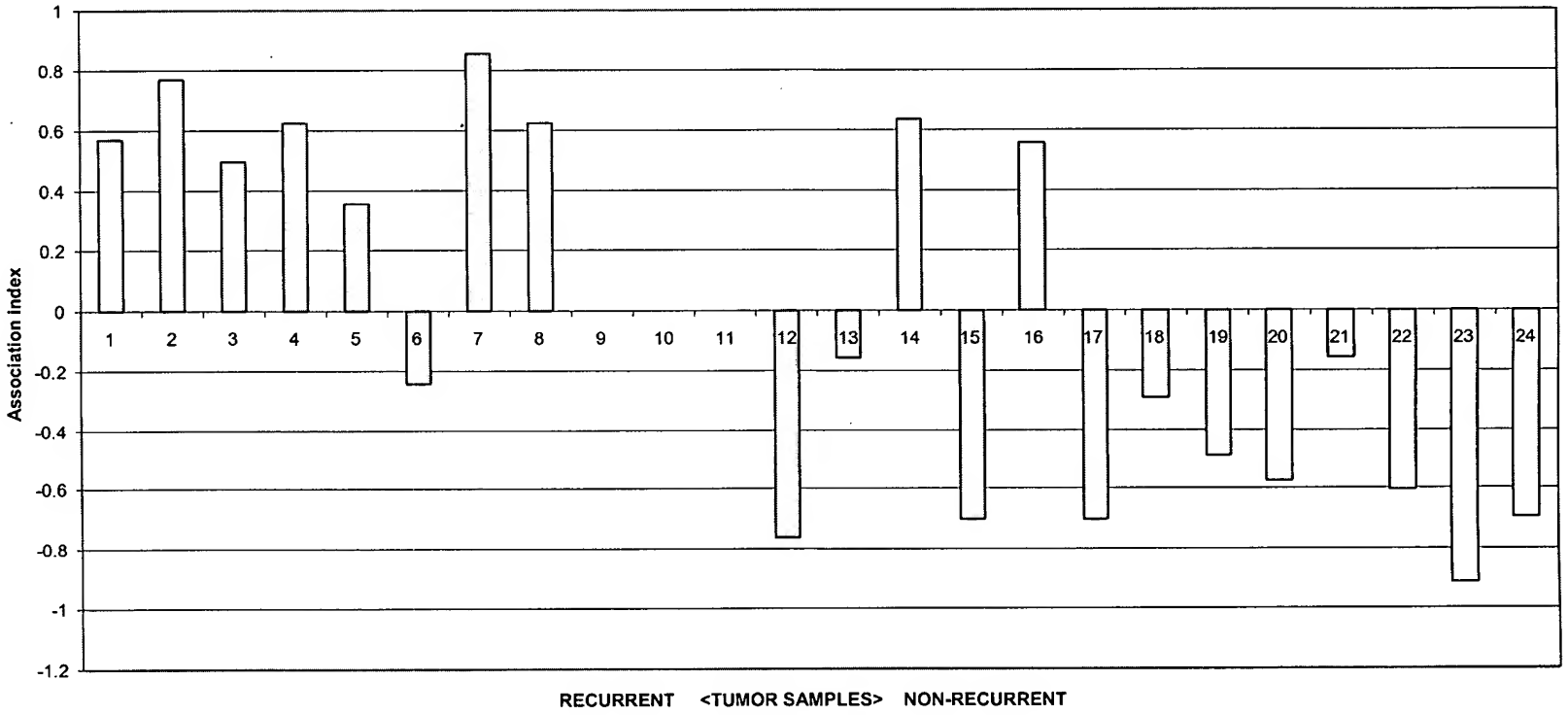


Figure 4. Phenotype association indexes for 54 genes of the prostate cancer/normal tissue discrimination class in 24 prostate tumors, 2 normal prostate stroma samples and 9 adjacent normal tissue samples

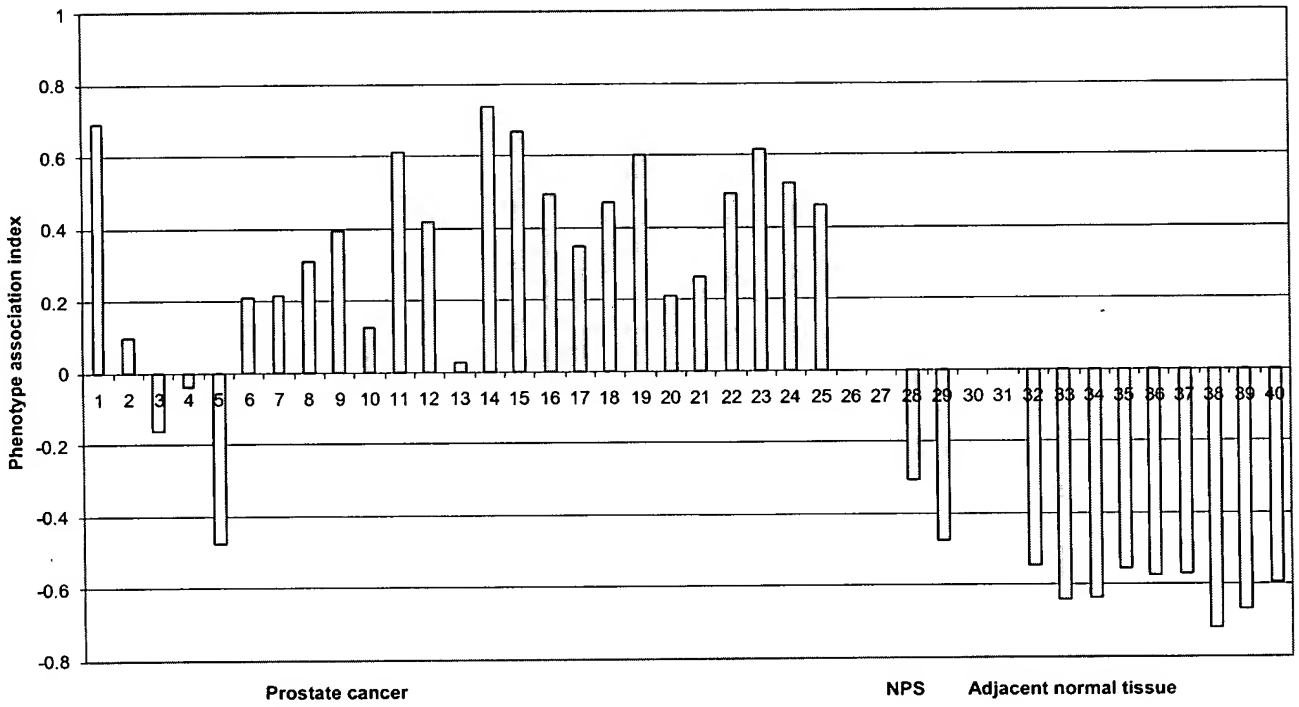


Figure 5. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 24 prostate cancer tissue samples versus 9 adjacent normal prostate samples for 54 genes of the concordant class

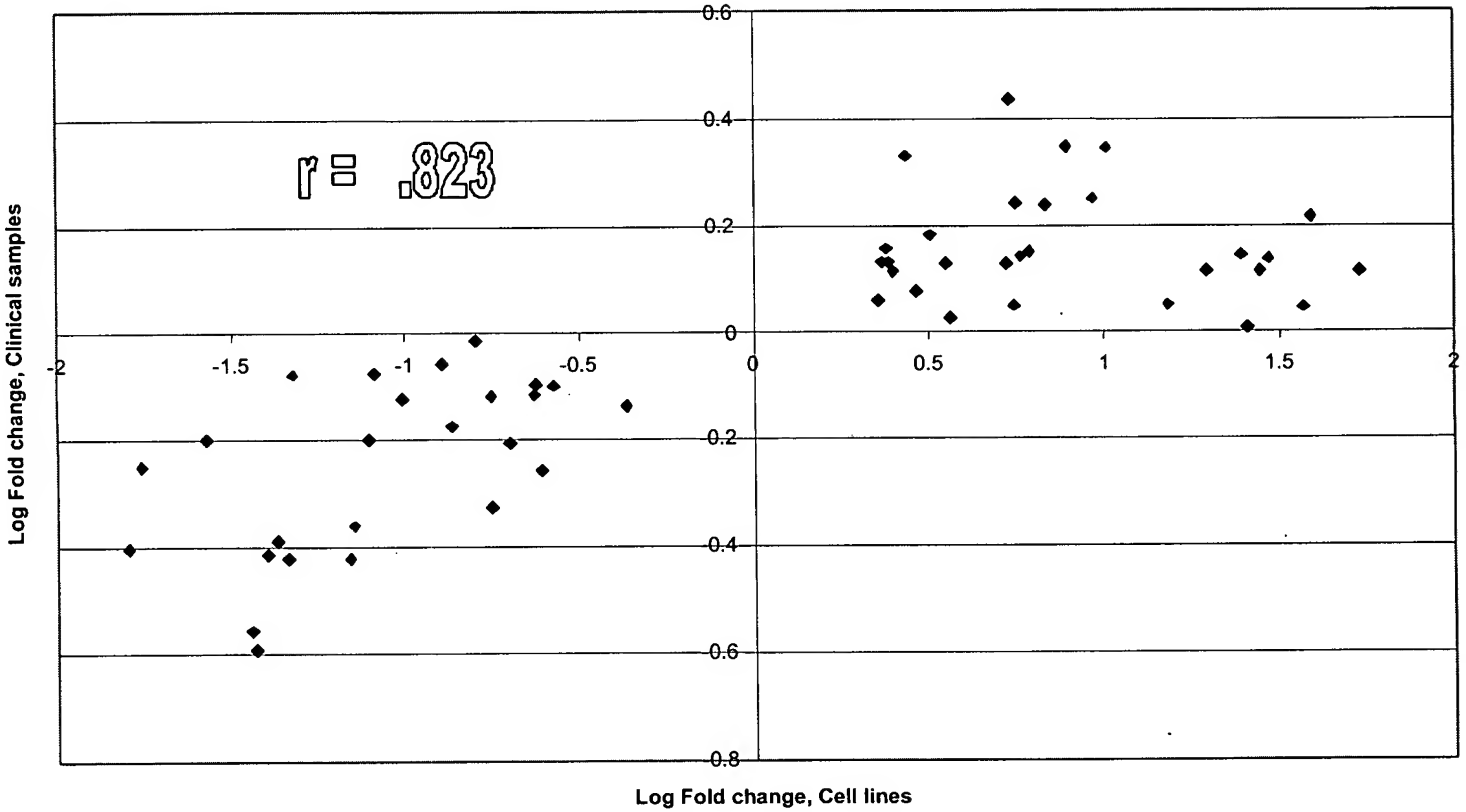


Figure 6. Phenotype association indexes for 10 genes of the prostate cancer/normal tissue discrimination class in 24 prostate tumors and 9 adjacent normal tissue samples

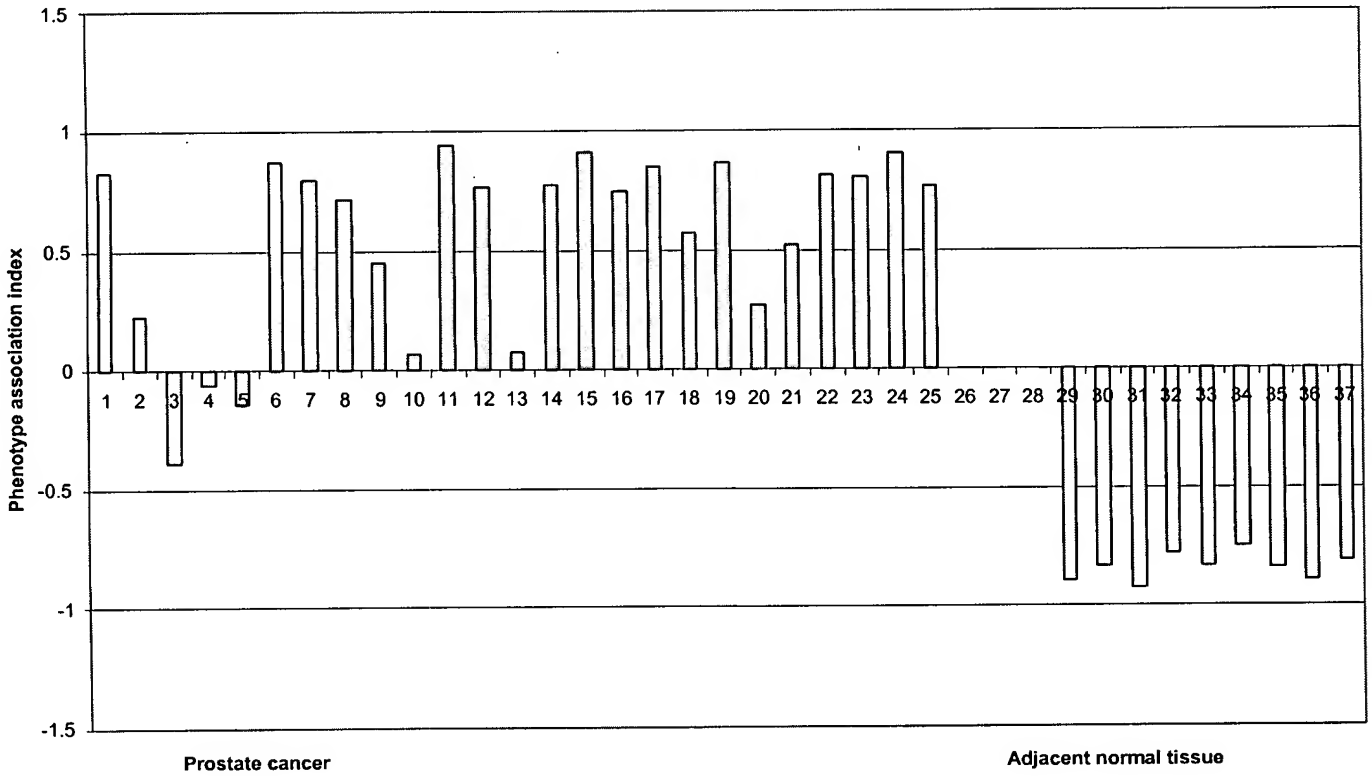


Figure 7. Phenotype association indexes for 5 genes of the prostate discrimination class in 24 prostate tumors and 9 adjacent normal

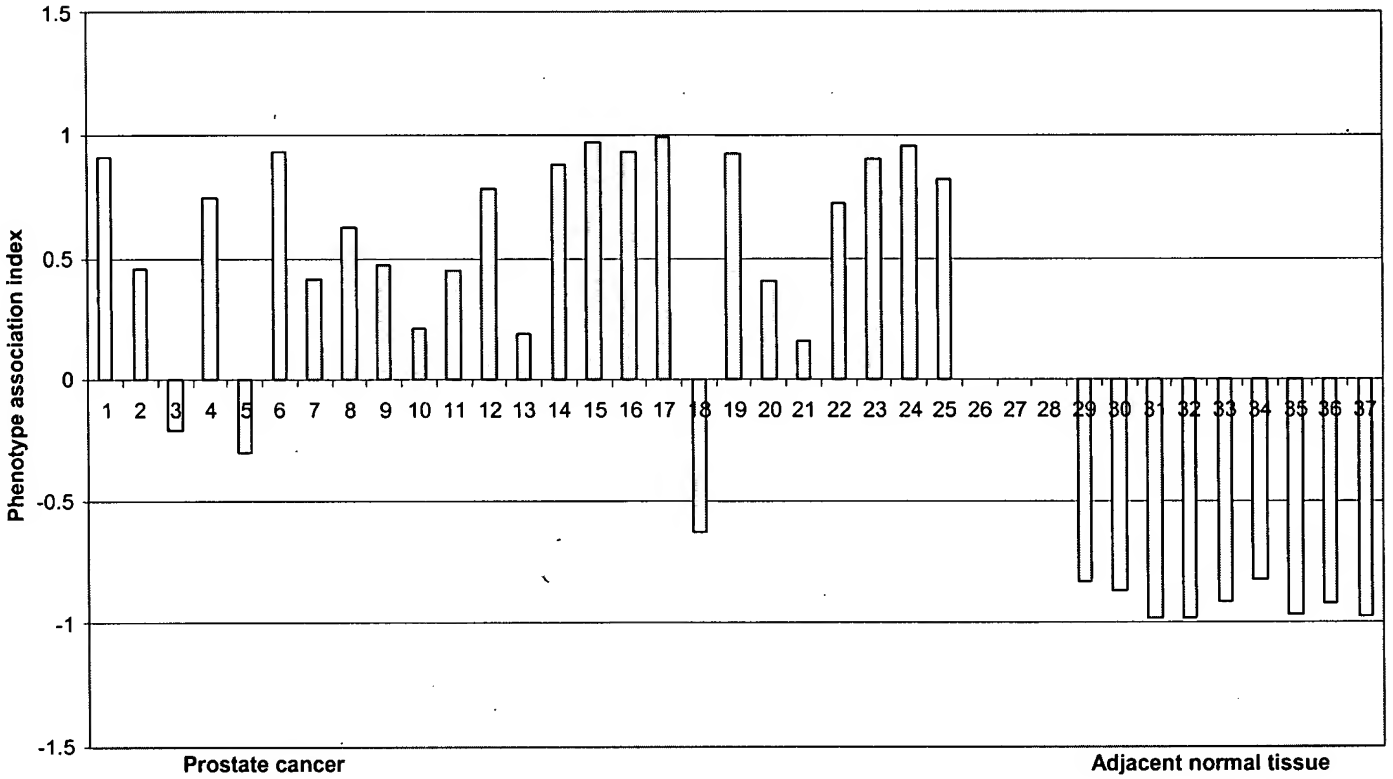


Figure 8. Phenotype association indexes for 10 genes of the prostate cancer/normal tissue discrimination class in 47 prostate tumors and 47 adjacent normal tissue samples

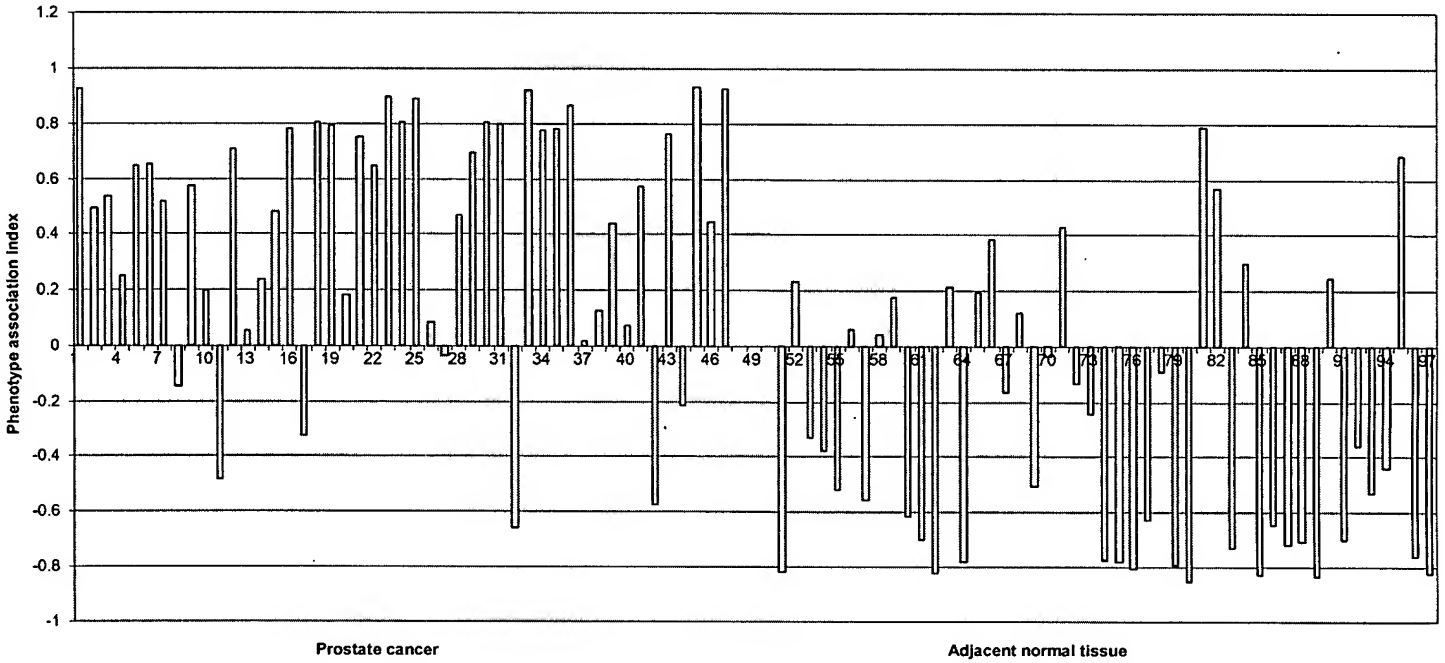


Figure 9. Phenotype association indexes for 5 genes of the prostate cancer/normal tissue discrimination class in 47 prostate tumors and 47 adjacent normal tissue samples

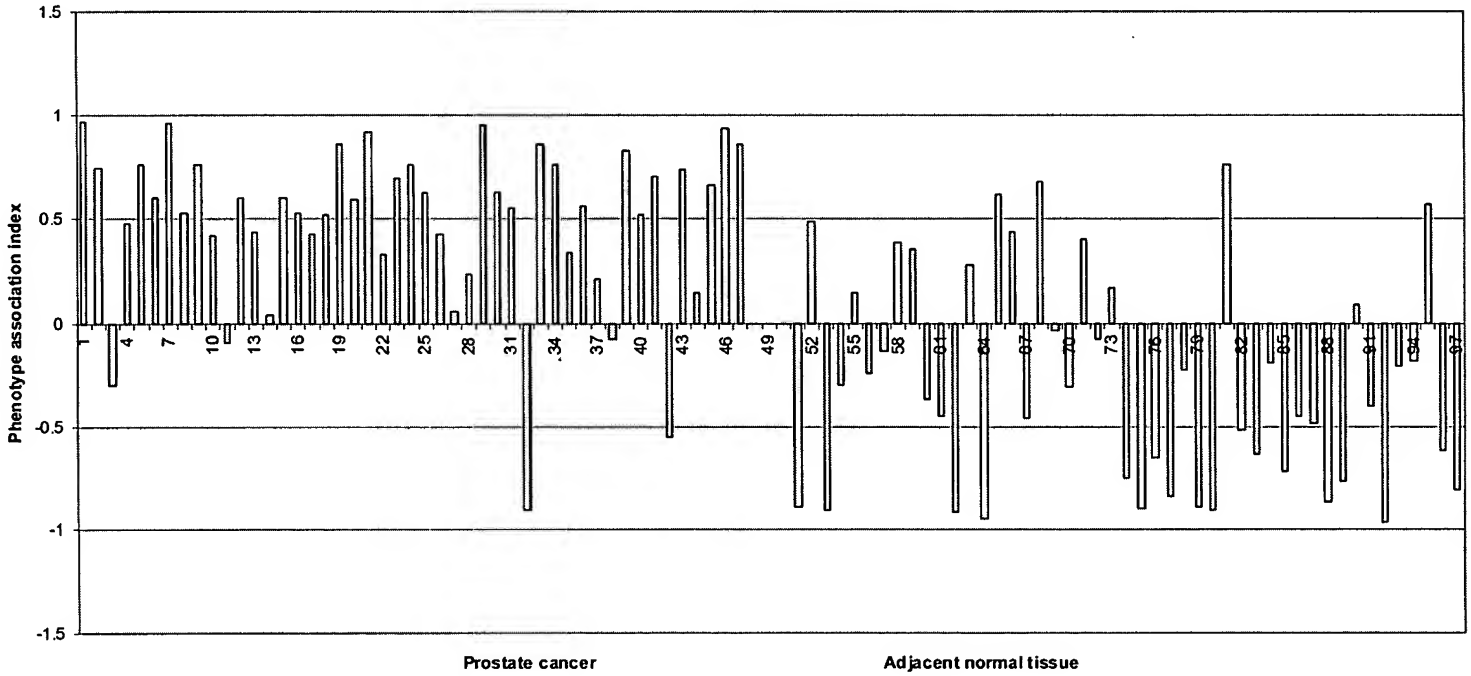


Figure 10. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 14 invasive versus 38 non-invasive human prostate tumors for 104 genes of the concordant class

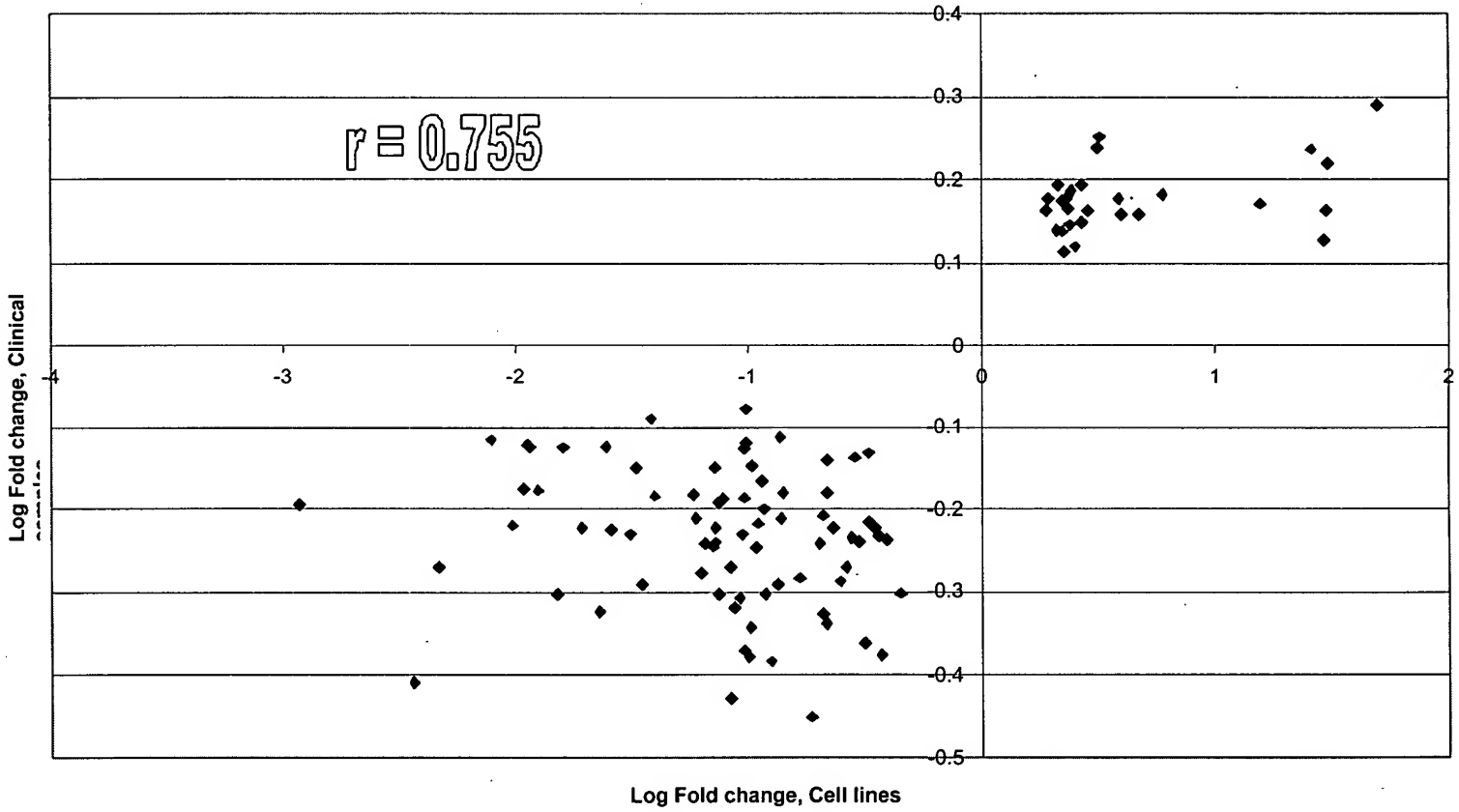


Figure 11. Correlation of the expression profiles in xenograft-derived human prostate carcinoma cell lines and 14 invasive versus 38 non-invasive human prostate tumors for 20 genes of the invasion minimum segregation class 1 (invasion cluster 1)

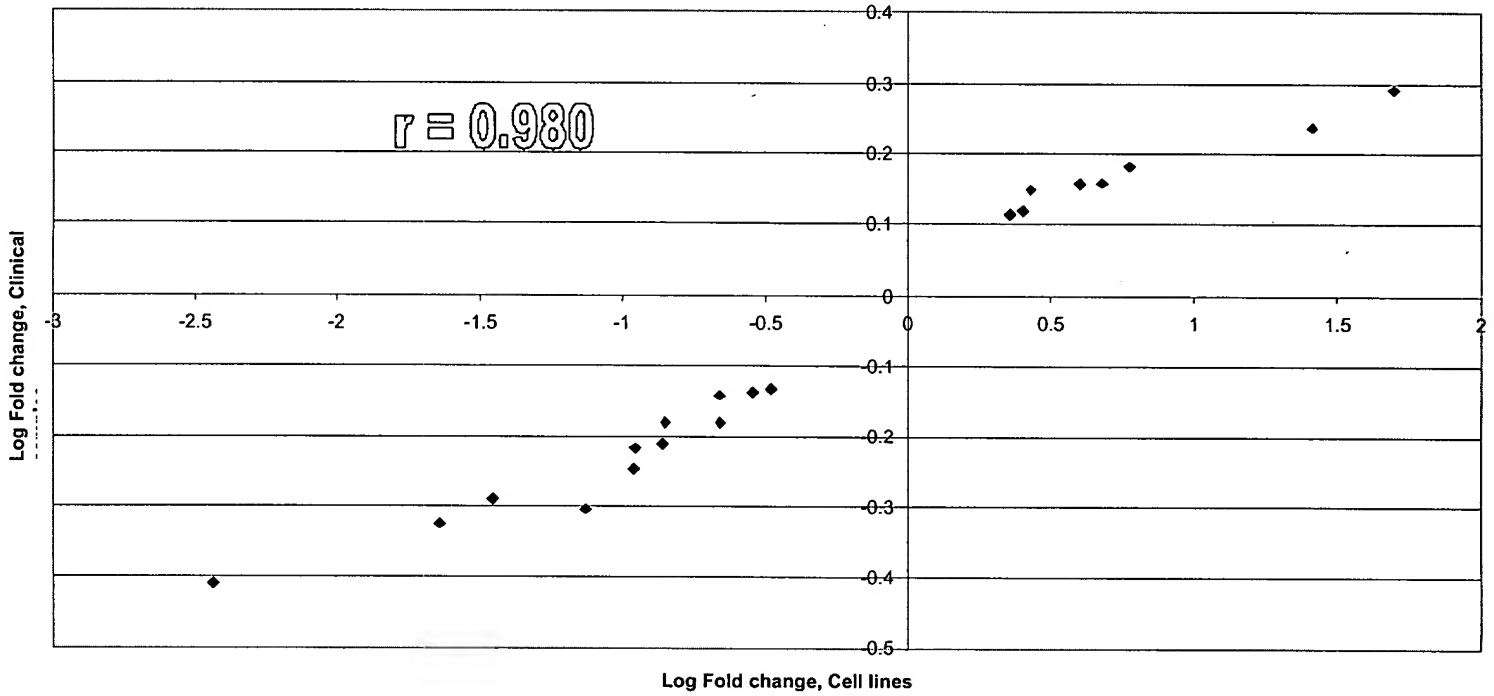


Figure 12. Phenotype association indexes in 14 invasive and 38 non-invasive human prostate tumors for 20 genes of the invasion cluster 1

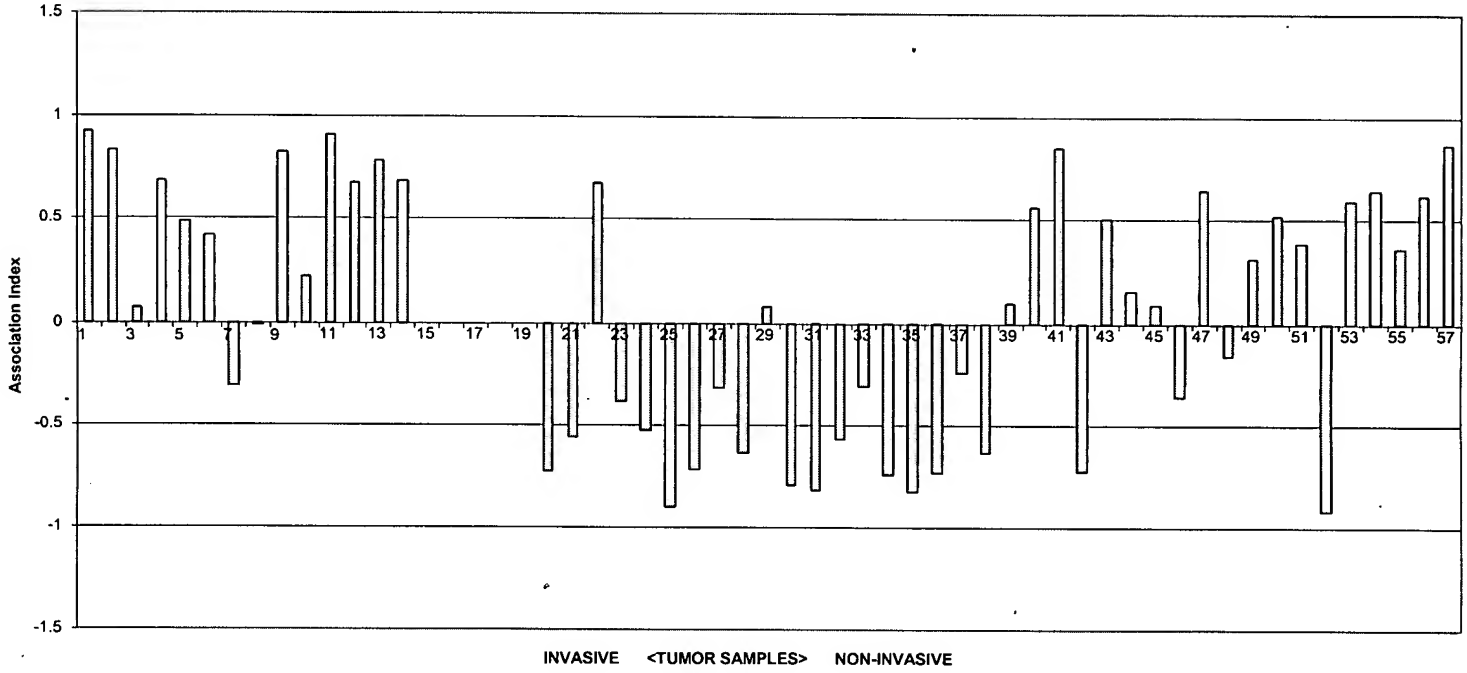


Figure 13. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 12 invasive versus 17 non-invasive human prostate tumors (surgical margins 1 +) for 12 genes of the invasion cluster 2

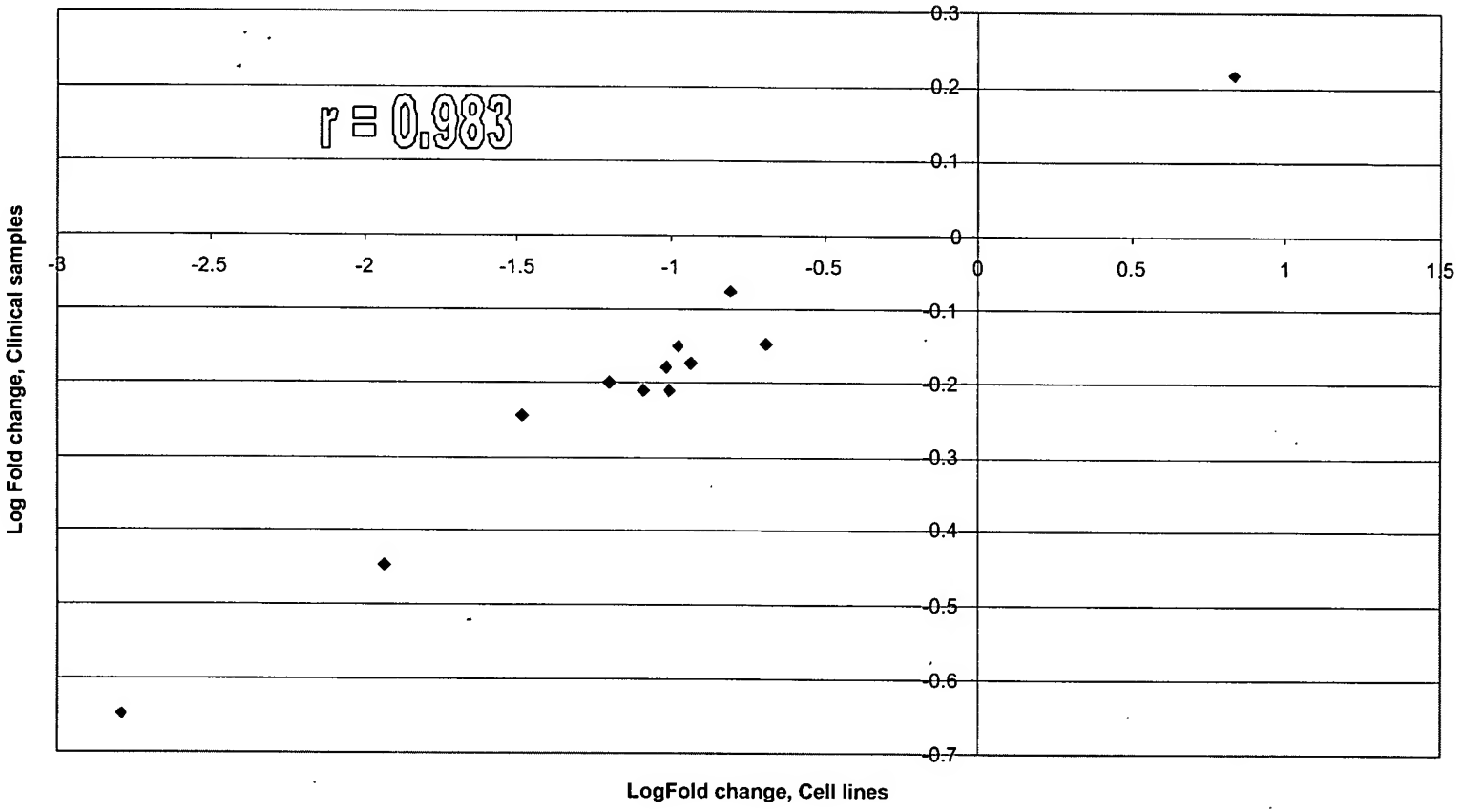


Figure 14. Phenotype association indexes in 12 invasive and 17 non-invasive human prostate tumors for 12 genes of the invasion cluster 2

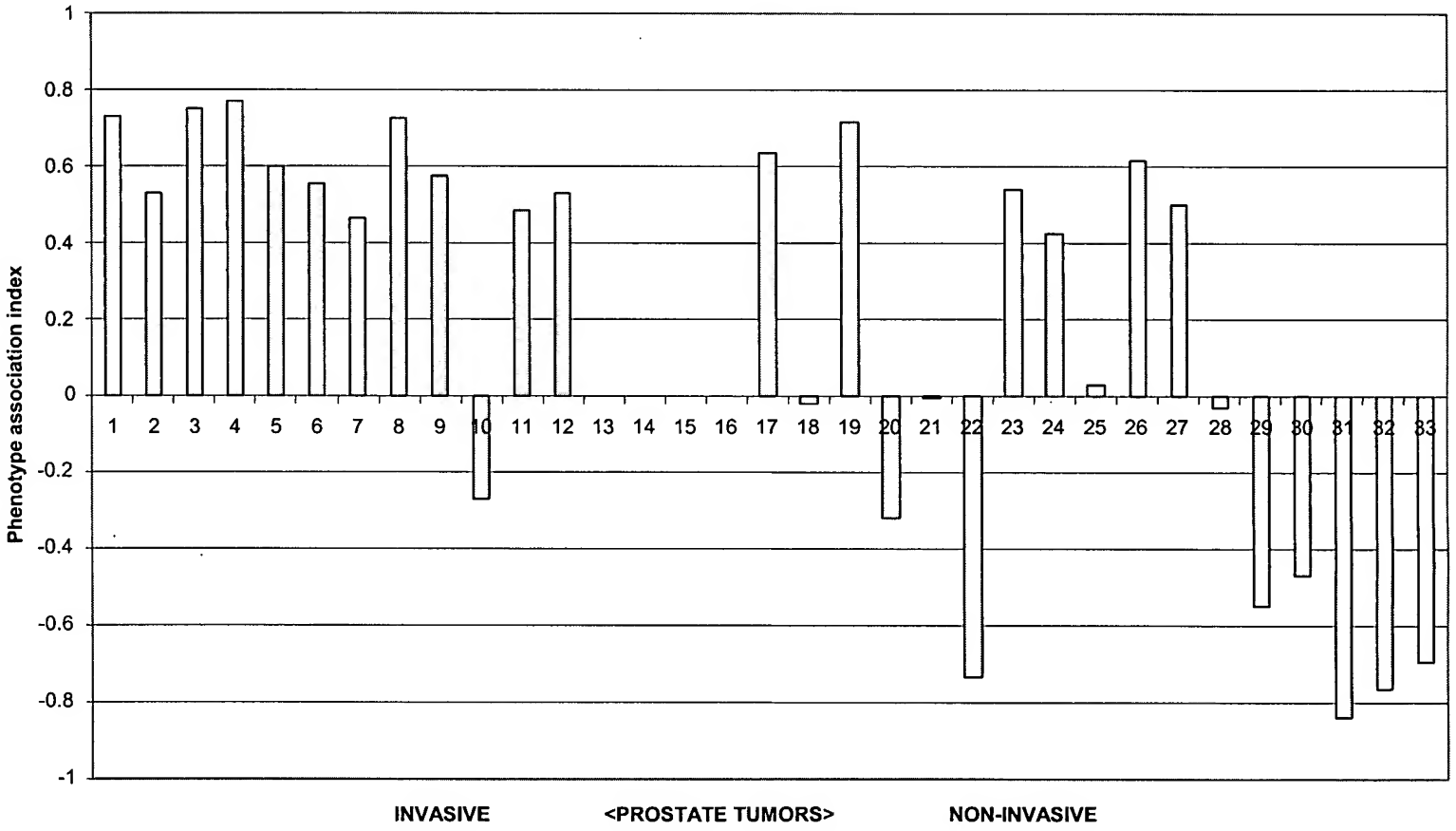


Figure 15. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 11 invasive versus 7 non-invasive human prostate tumors (invasion clusters 1 & 2 +) for 10 genes of the invasion cluster 3

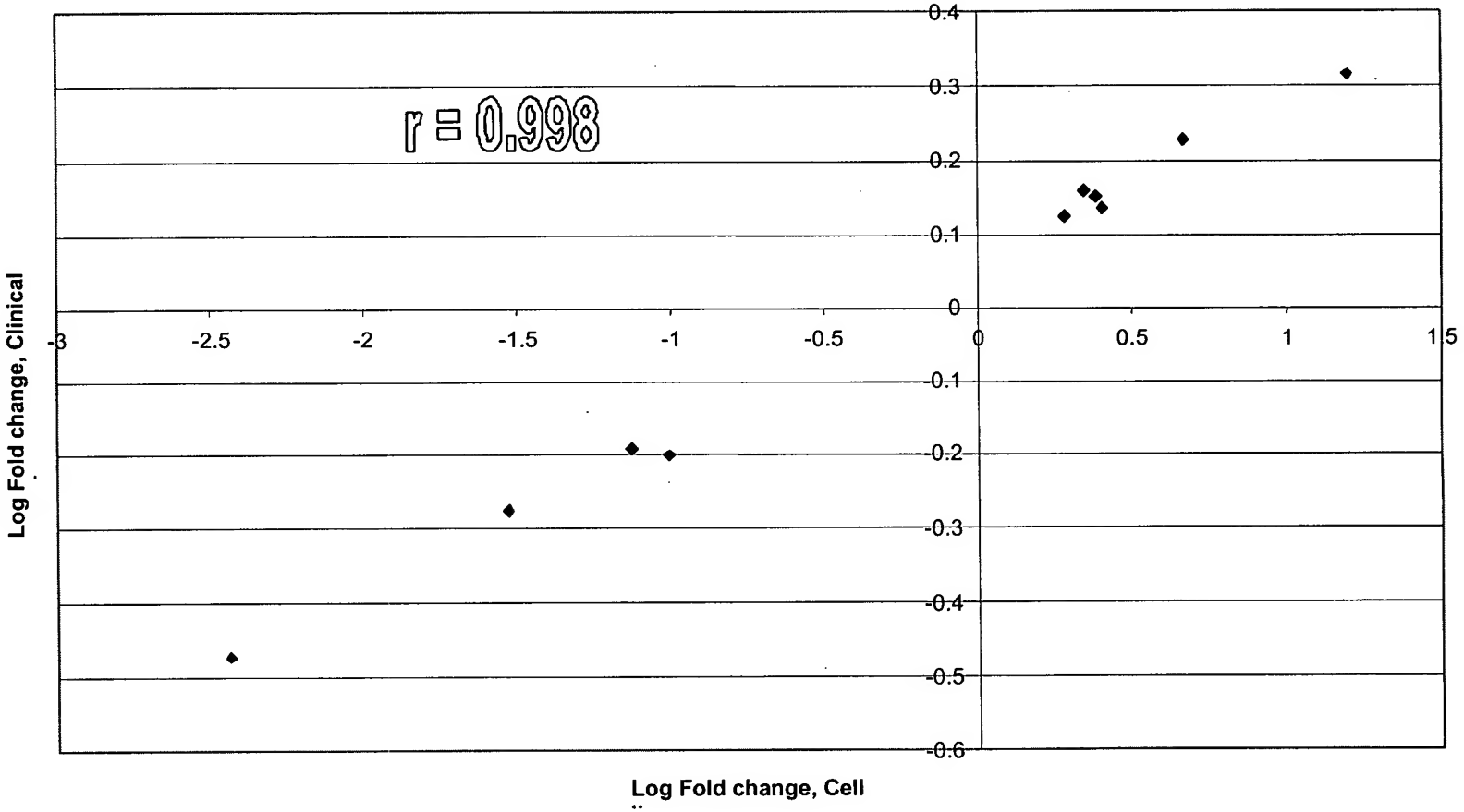


Figure 16. Phenotype association indexes in 11 invasive and 7 non-invasive human prostate tumors for 10 genes of the invasion cluster 3

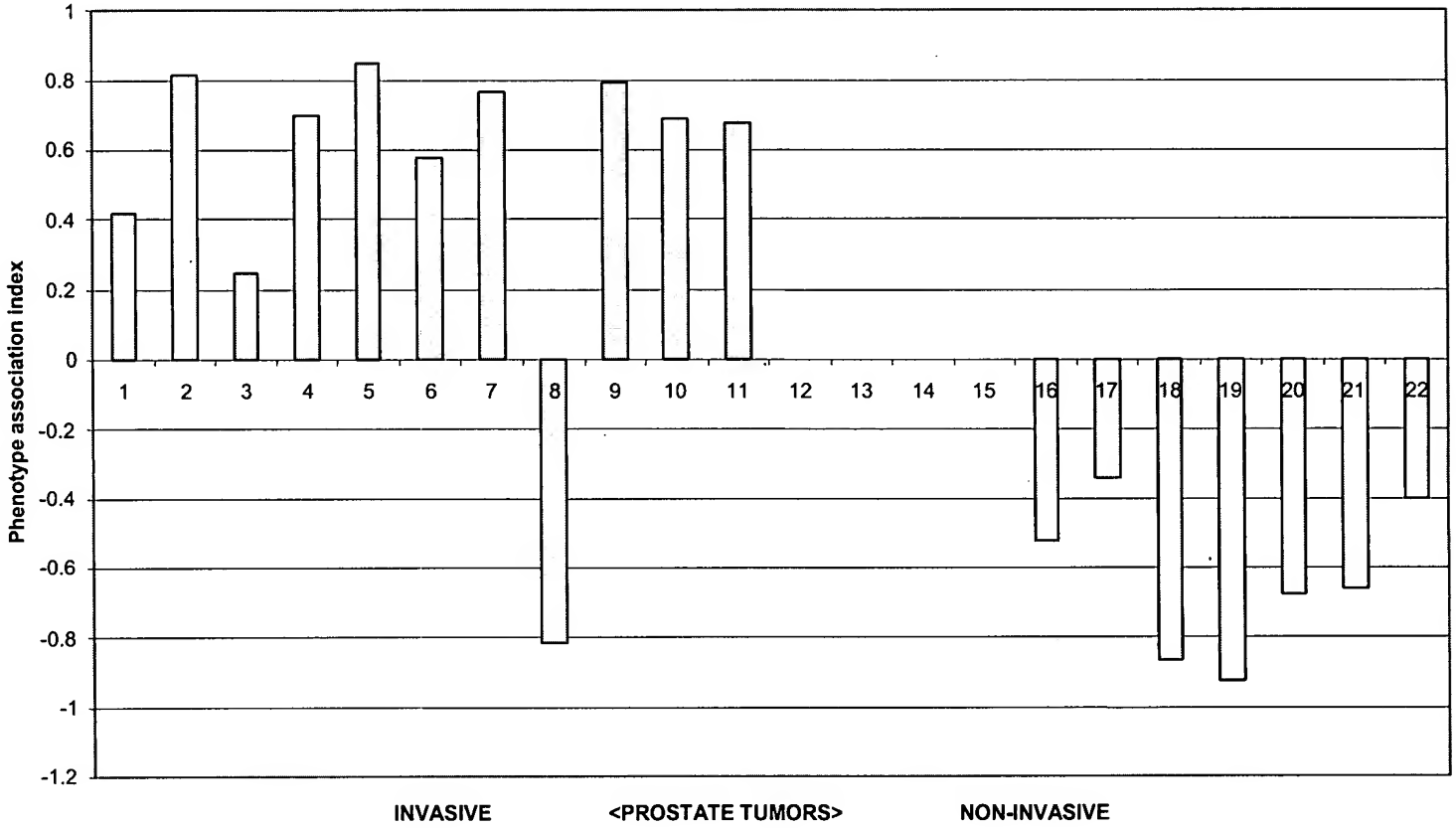


Figure 17. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 3 invasive versus 21 non-invasive human prostate tumors for 13 genes of the invasion cluster 4.

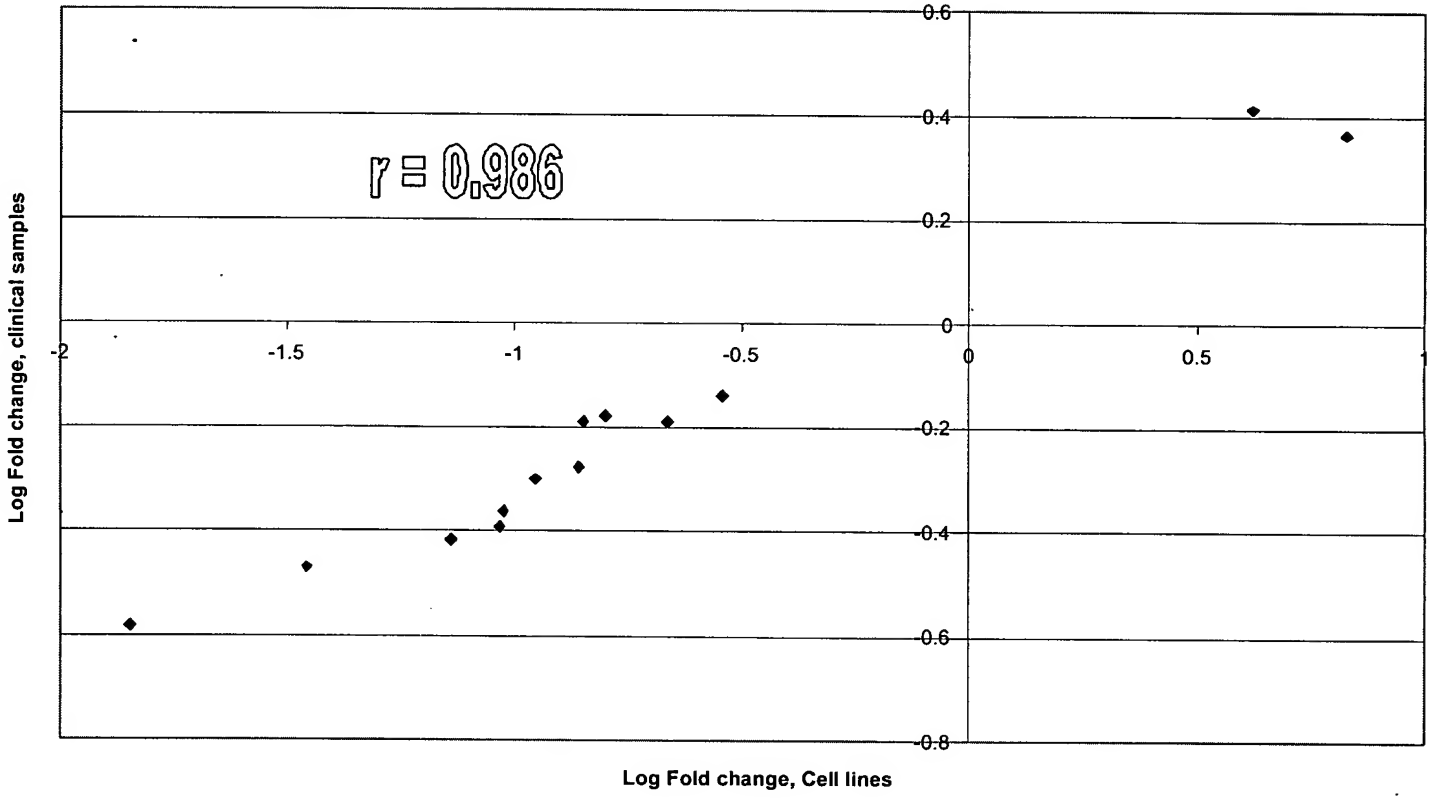


Figure 18. Phenotype association indexes in 3 invasive and 21 non-invasive human prostate tumors for 13 genes of the invasion cluster 4

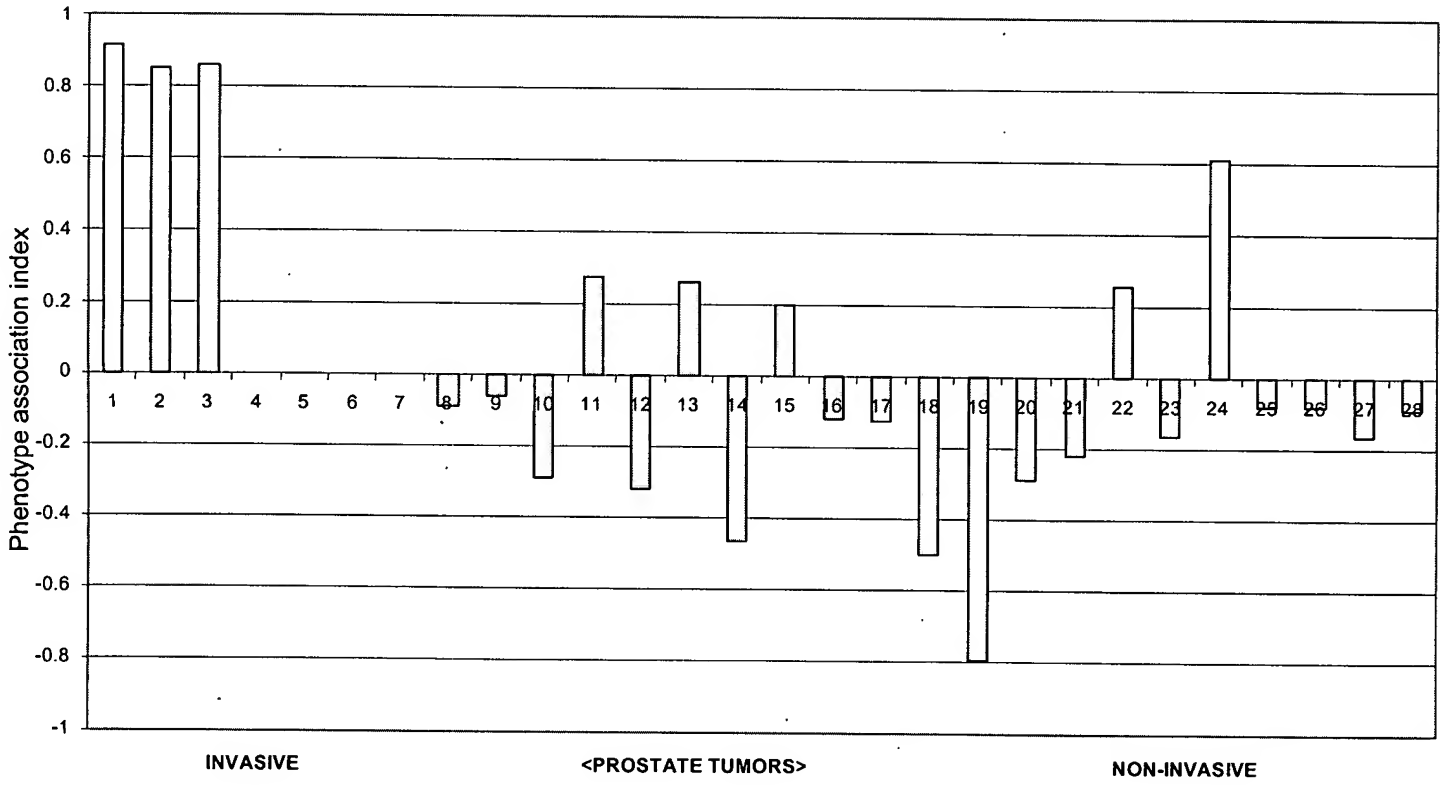


Figure 19. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 6 high Gleason grade versus 46 low Gleason grade prostate tumors for 58 genes of the concordant class

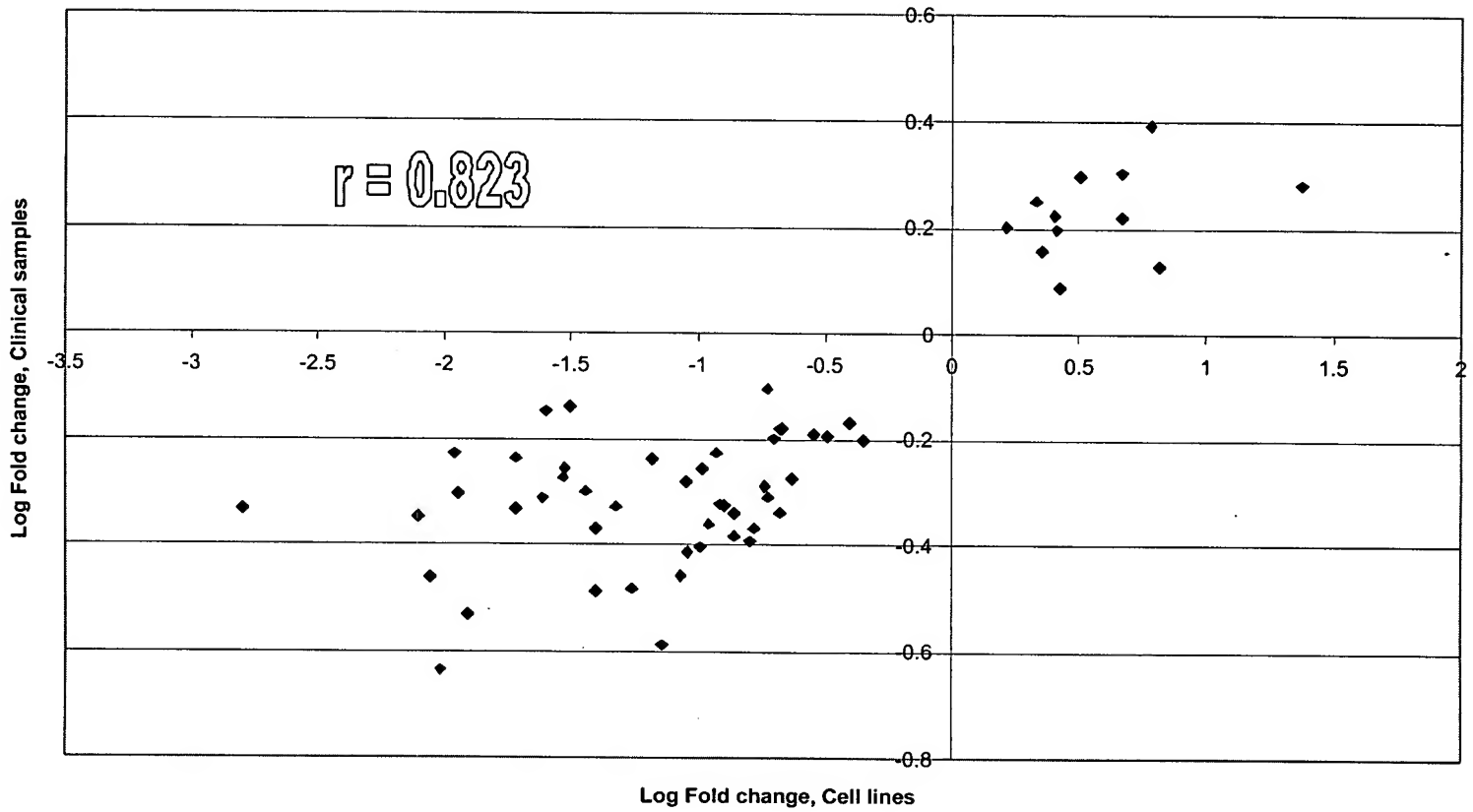


Figure 20. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 6 high Gleason grade versus 46 low Gleason grade prostate tumors for 17 genes high grade cluster 1

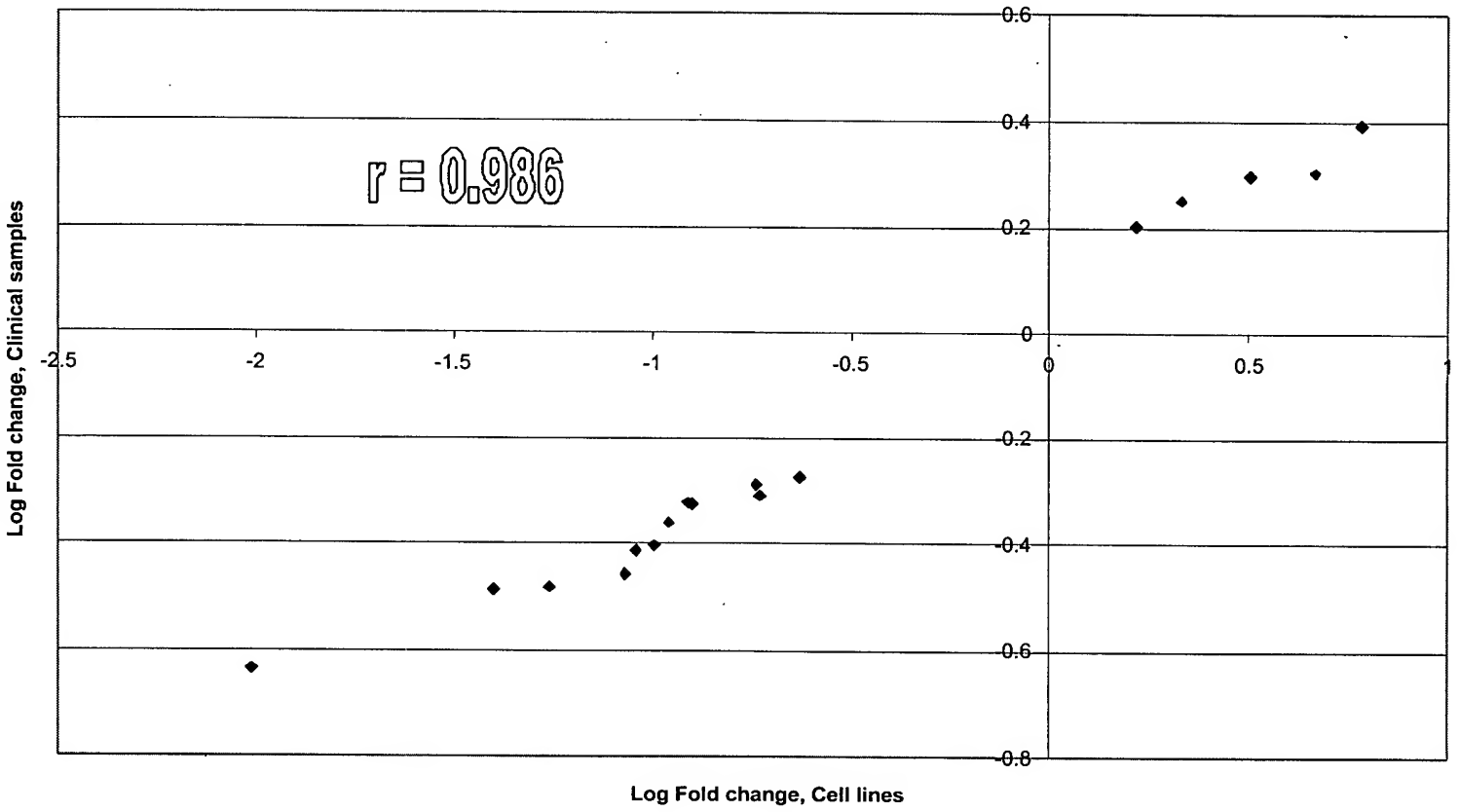


Figure 21. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 6 high Gleason grade versus 20 low Gleason grade prostate tumors for 12 genes high grade cluster 2

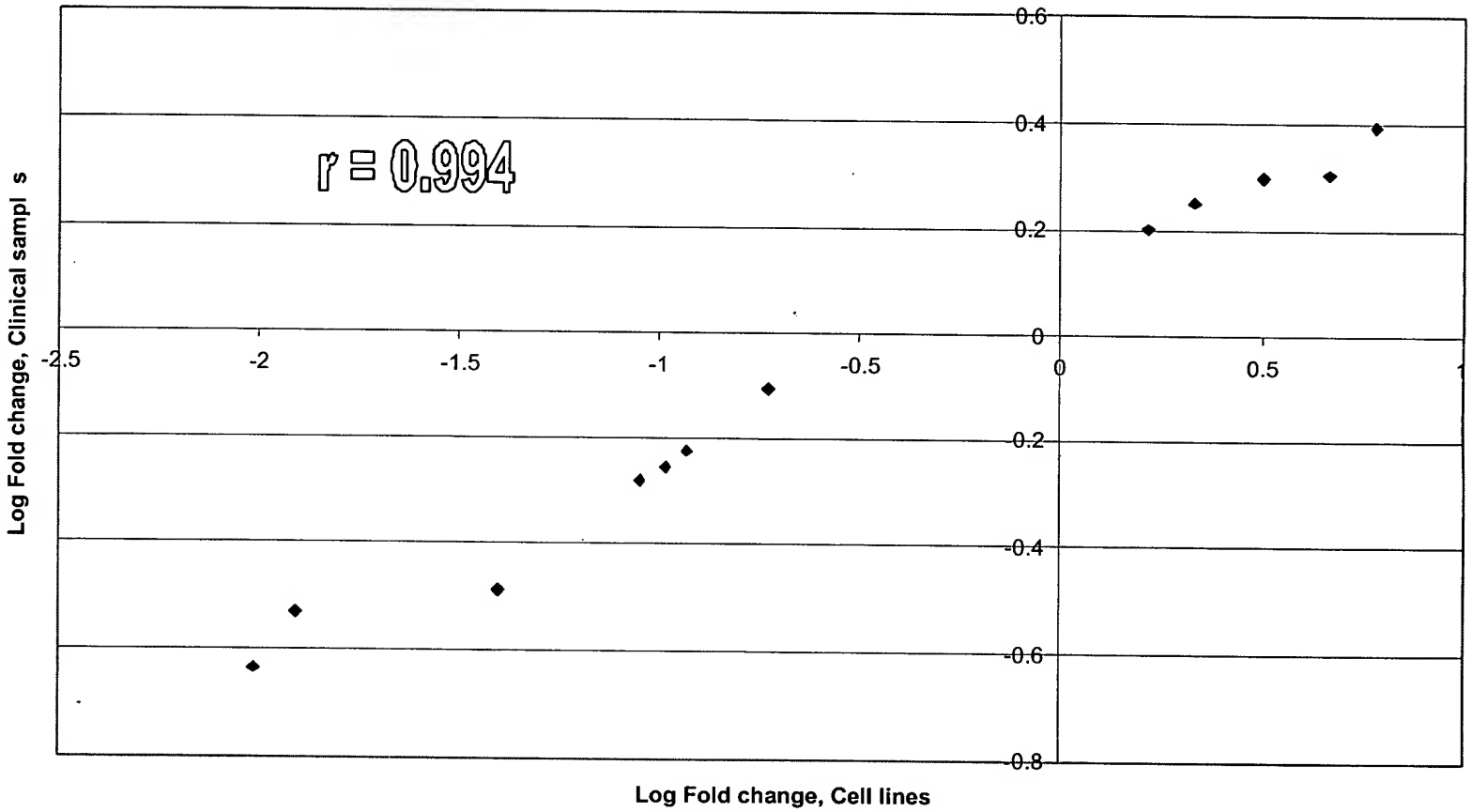


Figure 22. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 6 high Gleason grade versus 16 low Gleason grade prostate tumors for 7 genes high grade cluster 3

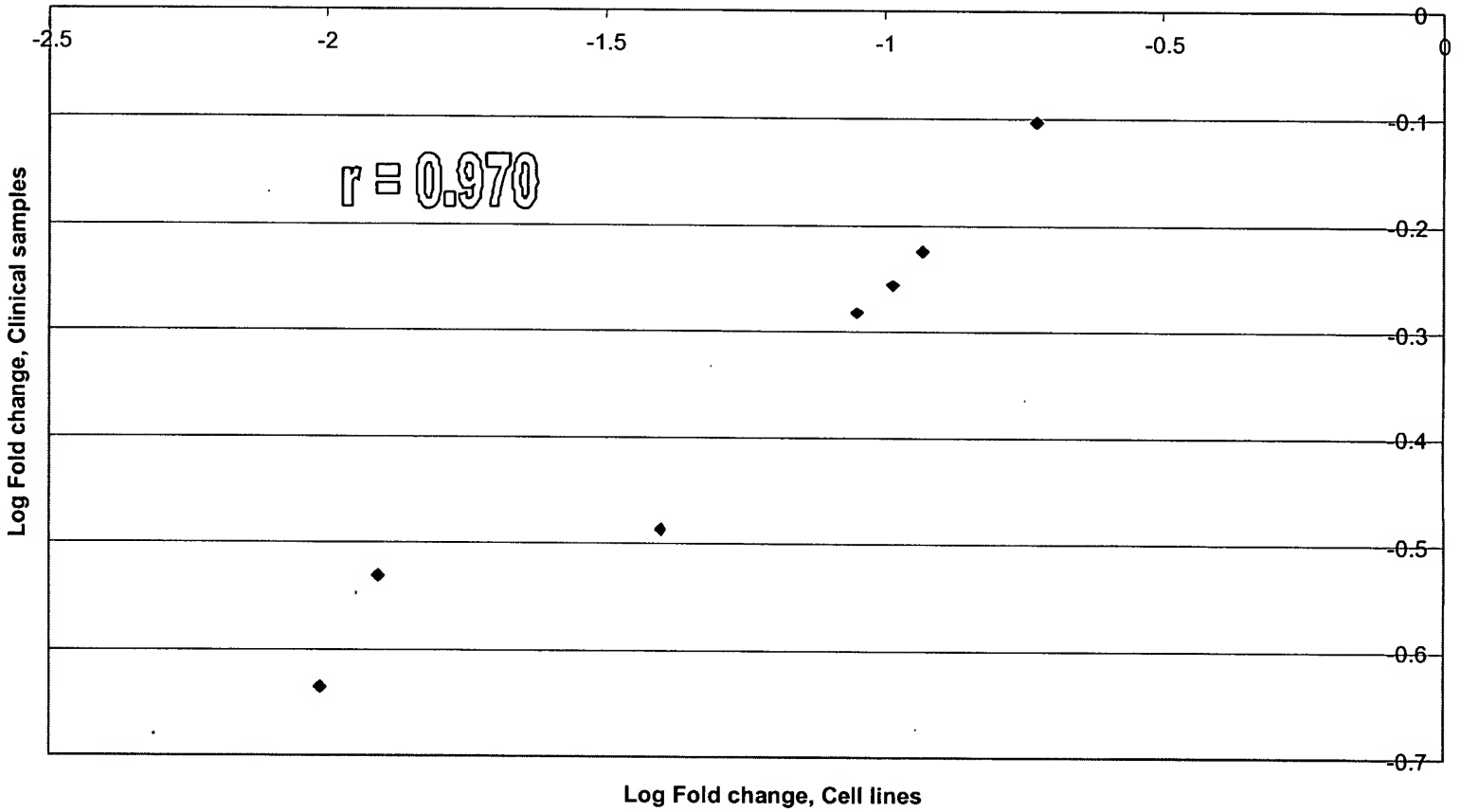


Figure 23. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 6 high Gleason grade versus 46 low Gleason grade prostate tumors for 38 genes of the ALT high grade cluster

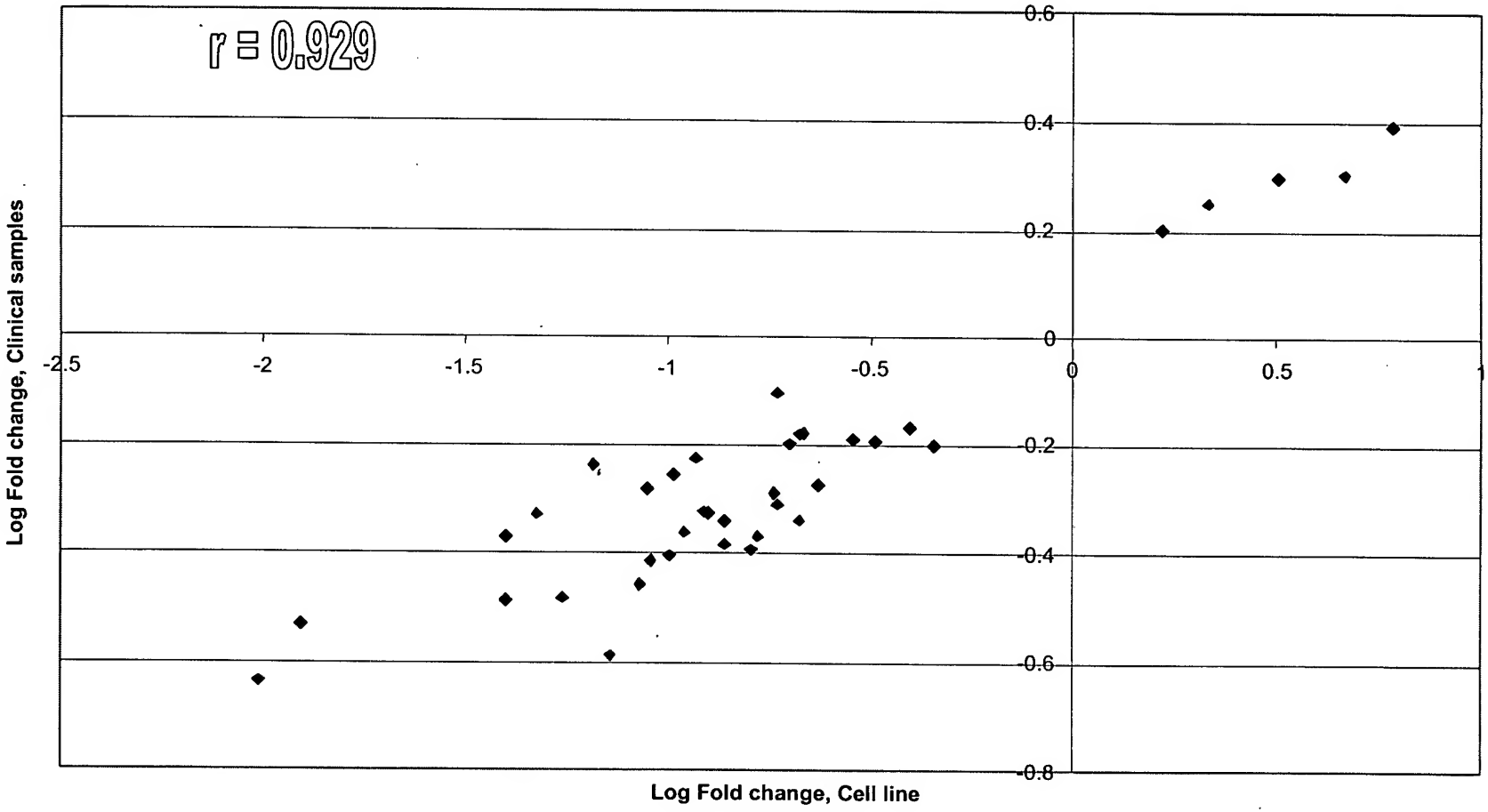


Figure 24. Correlation of the expression profiles in 5 xenograft-derived carcinoma cell lines and 6 high Gleason grade versus 17 low Gleason grade for 5 genes high grade cluster 4

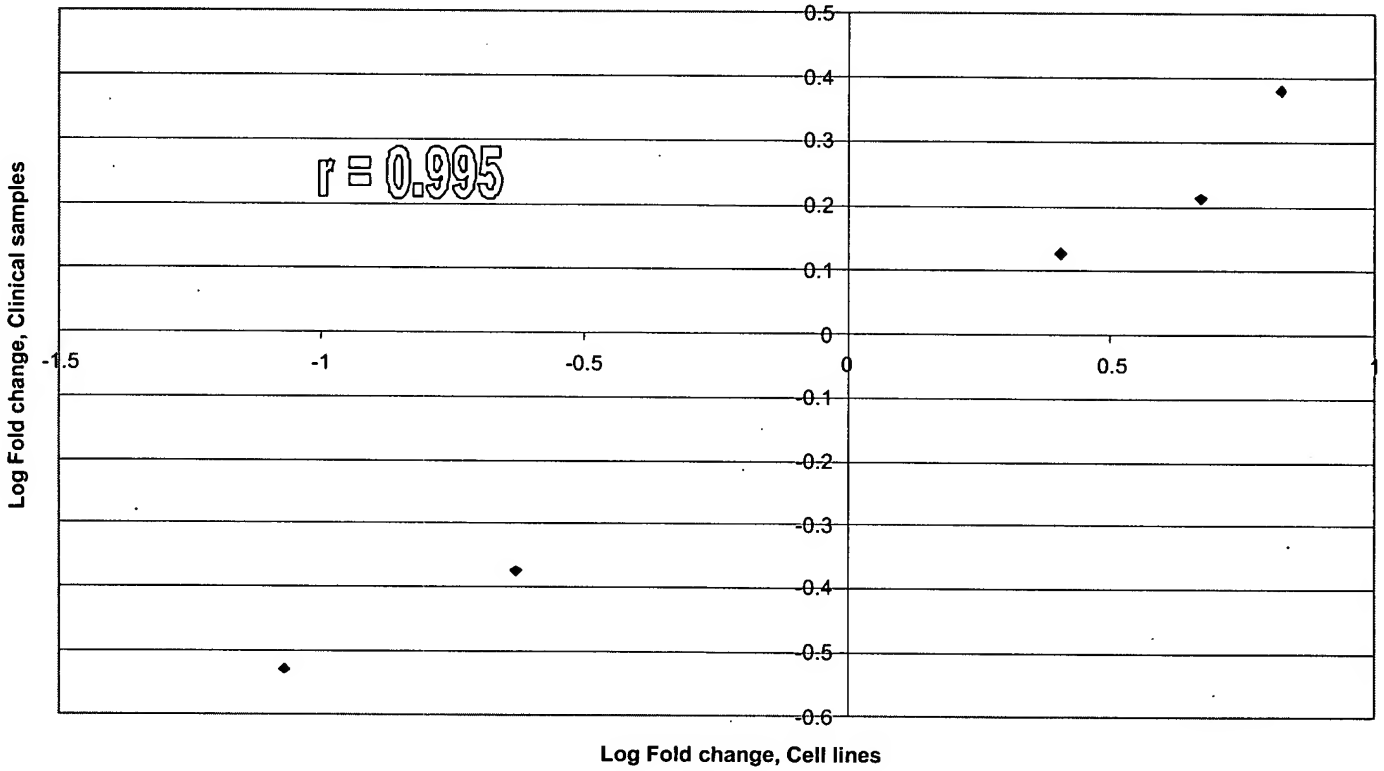


Figure 25. Correlation of the expression profiles in 5 xenograft-derived human carcinoma cell lines and 6 high Gleason grade versus 17 low Gleason grade prostate for 4 genes high grade cluster 5

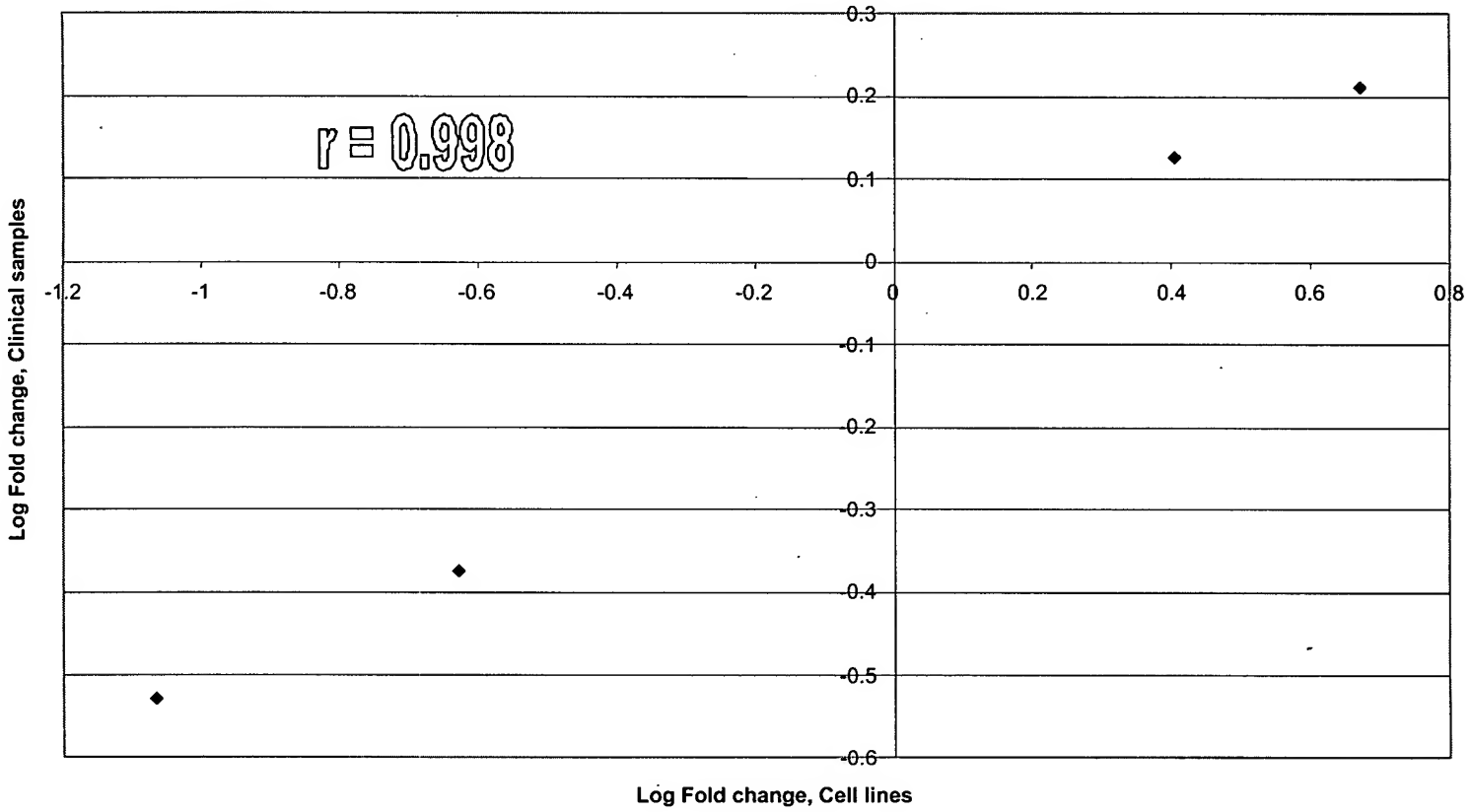


Figure 26. Correlation of the expression profiles in 5 xenograft-derived human carcinoma cell lines and 6 high Gleason grade versus 17 low Gleason grade prostate for 7 genes high grade cluster 6

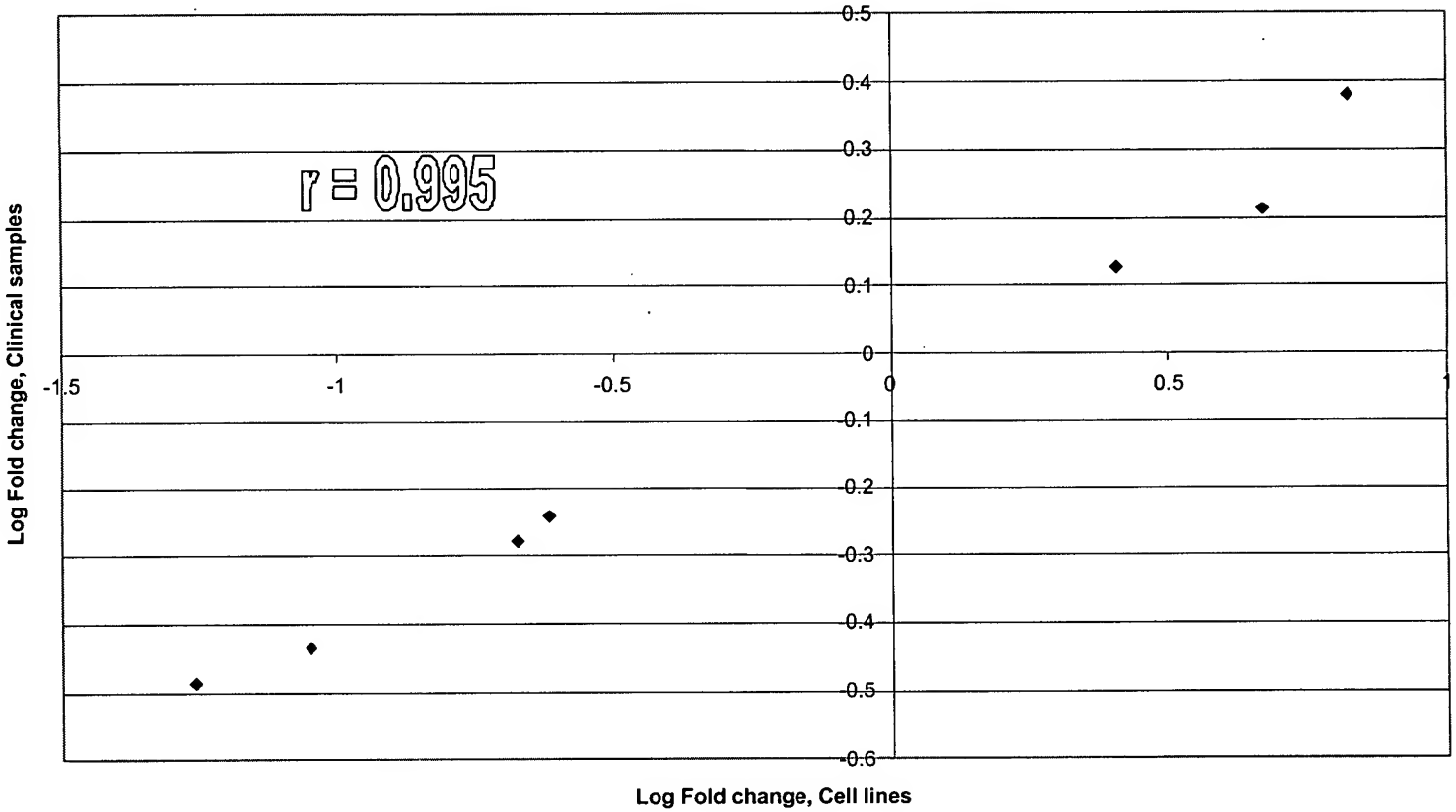


Figure 27. Correlation of the expression profiles in 5 xenograft-derived human prostate carcinoma cell lines and 6 high Gleason grade versus 17 low Gleason grade prostate tumors for 13 genes high grade cluster 7

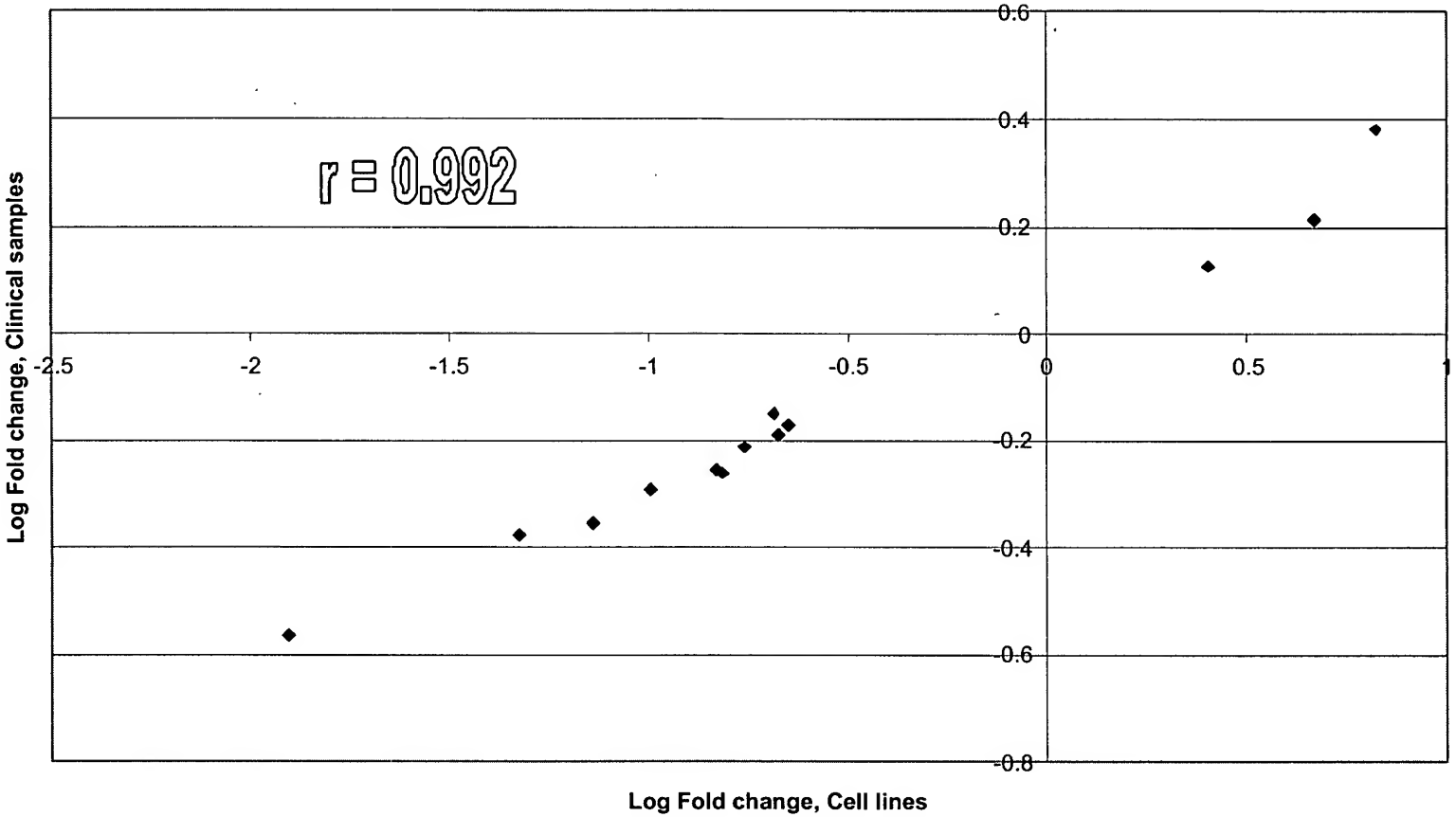


Figure 28. Phenotype association indexes for 54 genes of the BPH segregation cluster in 8 patients with BPH and 9 patients with prostate cancer

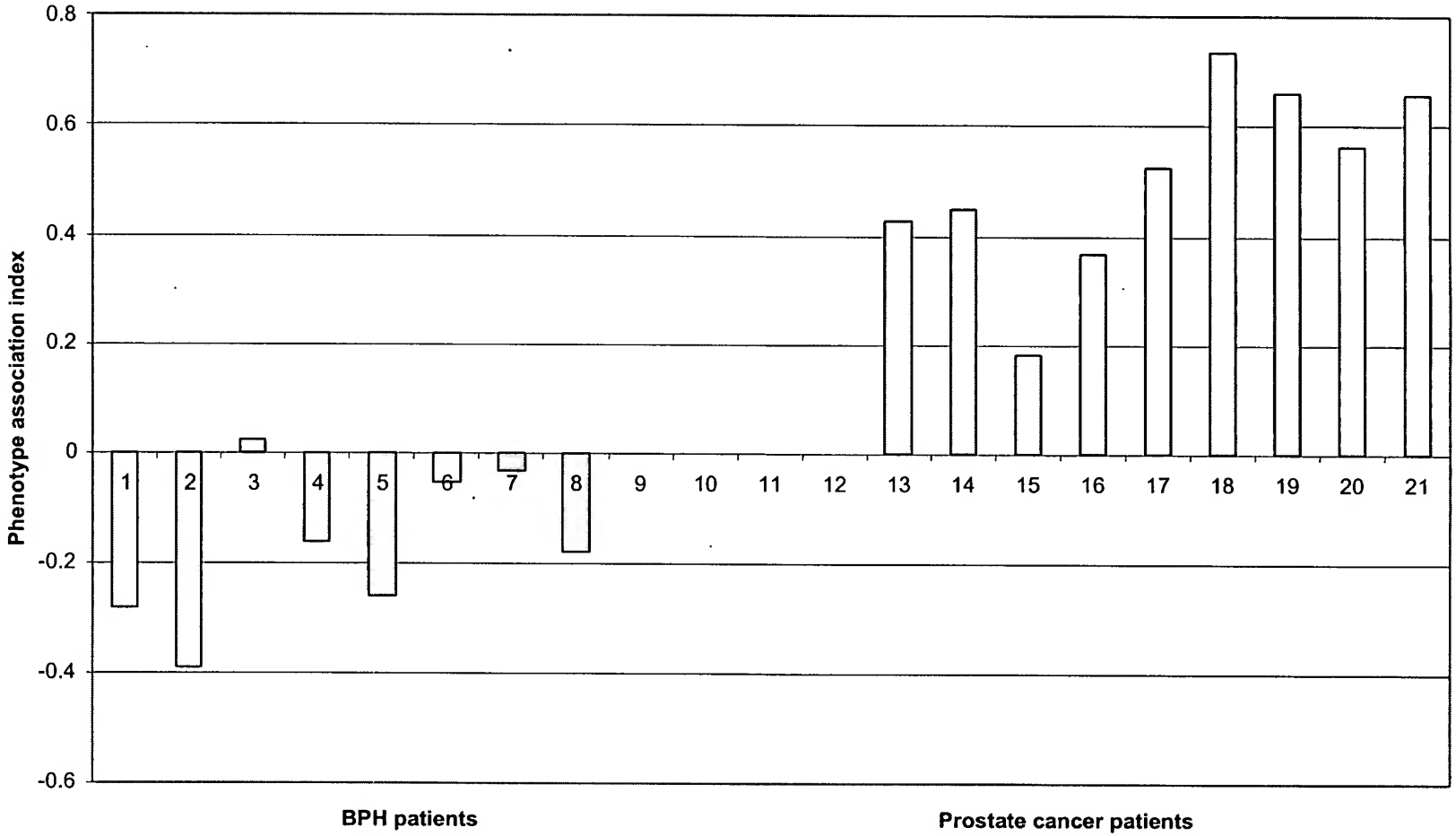


Figure 29. Phenotype association indexes for 14 genes of the BPH segregation cluster MAGEA1 in 8 patients with BPH and 9 patients with prostate cancer

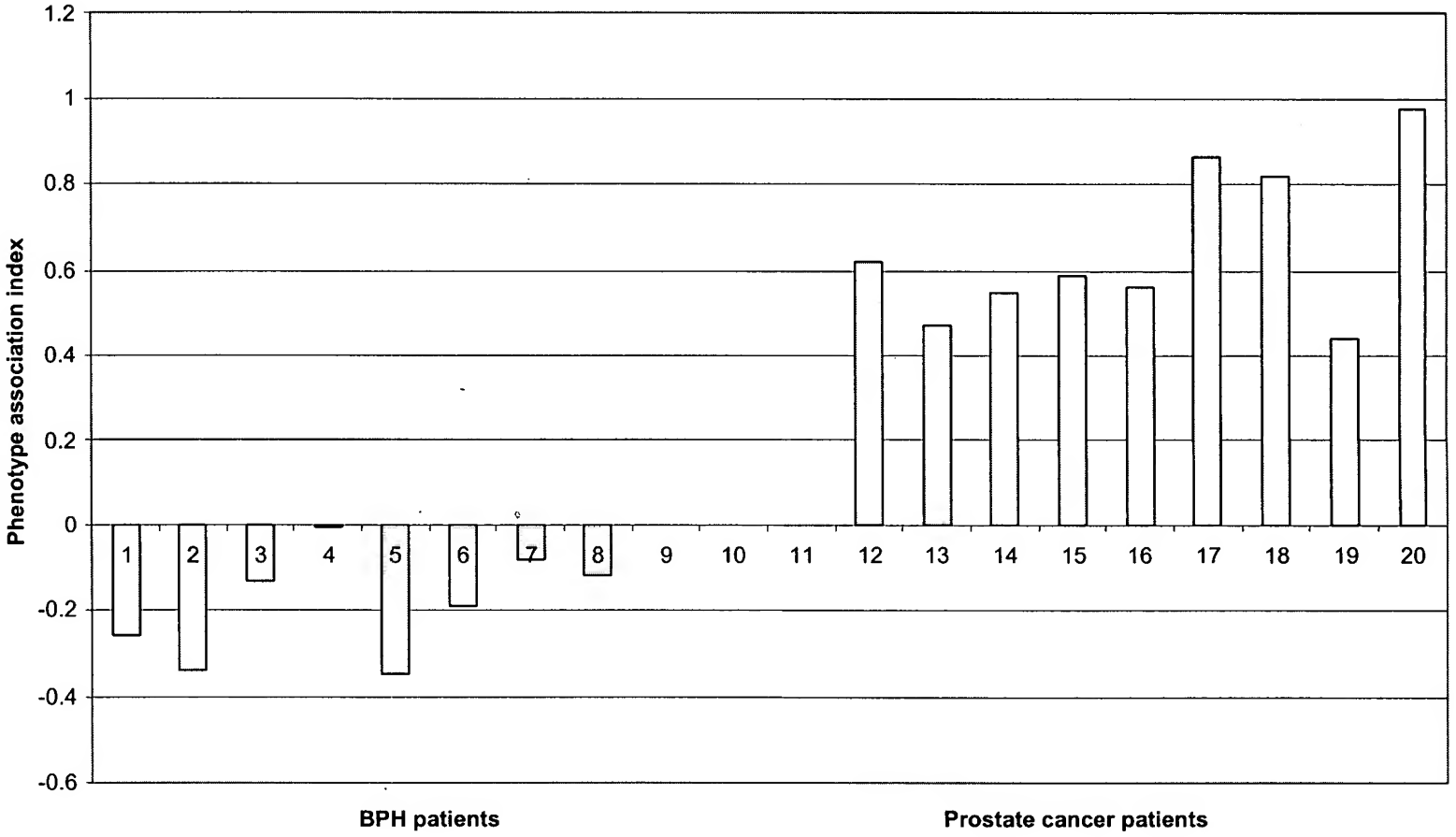


Figure 30. Phenotype association indices for 17 genes of metastasis seggregation class 1 in 5 BPH samples, 3 ANP samples, prostatitis, 10 samples of localized prostate cancer (LPC), and 7 samples of metastatic prostate cancer (MPC)

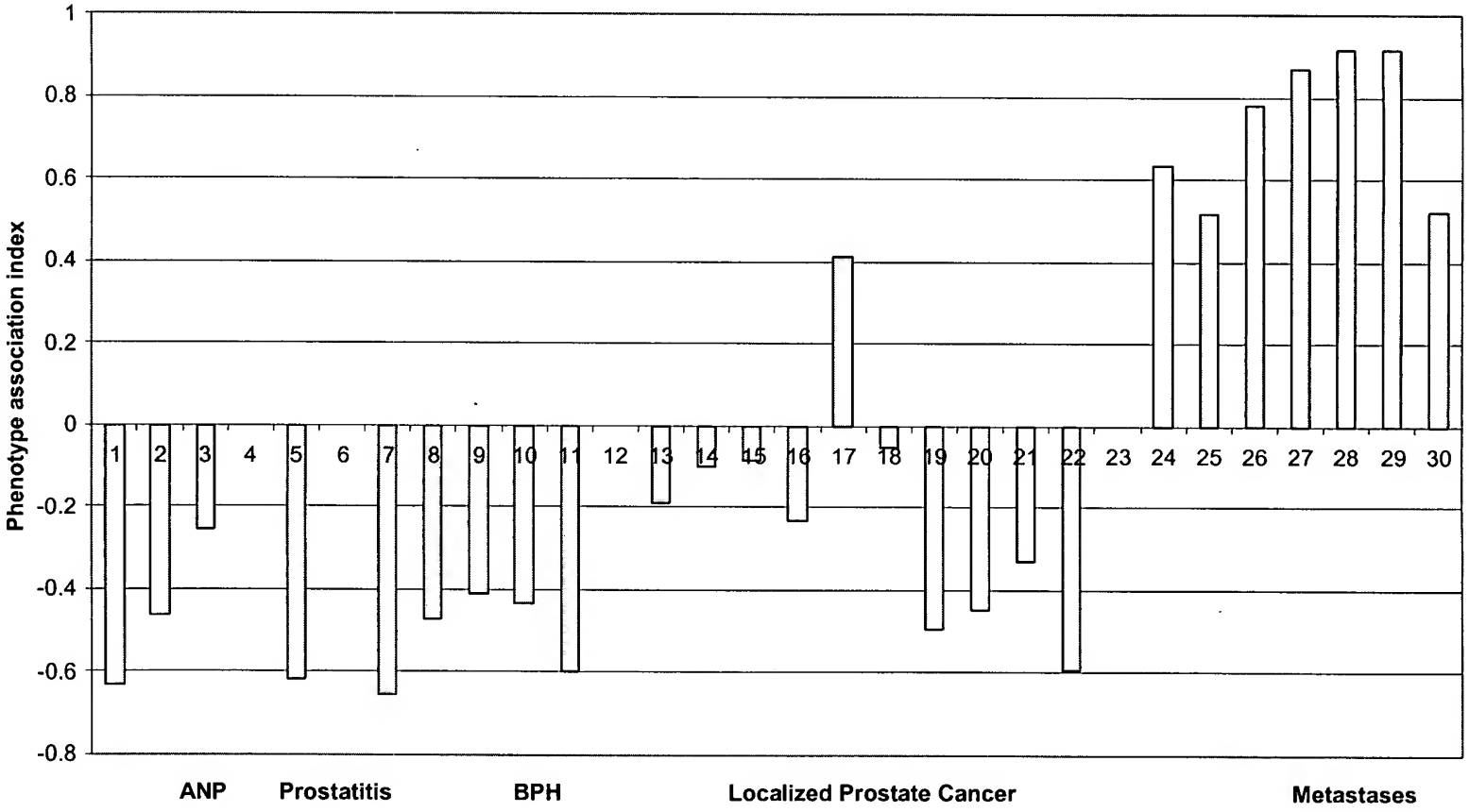


Figure 31. Phenotype association indices for 19 genes of metastasis seggregation class 2 in 5 BPH samples, 3 ANP samples, prostatitis, 10 samples of localized prostate cancer (LPC), and 7 samples of metastatic prostate cancer (MPC)

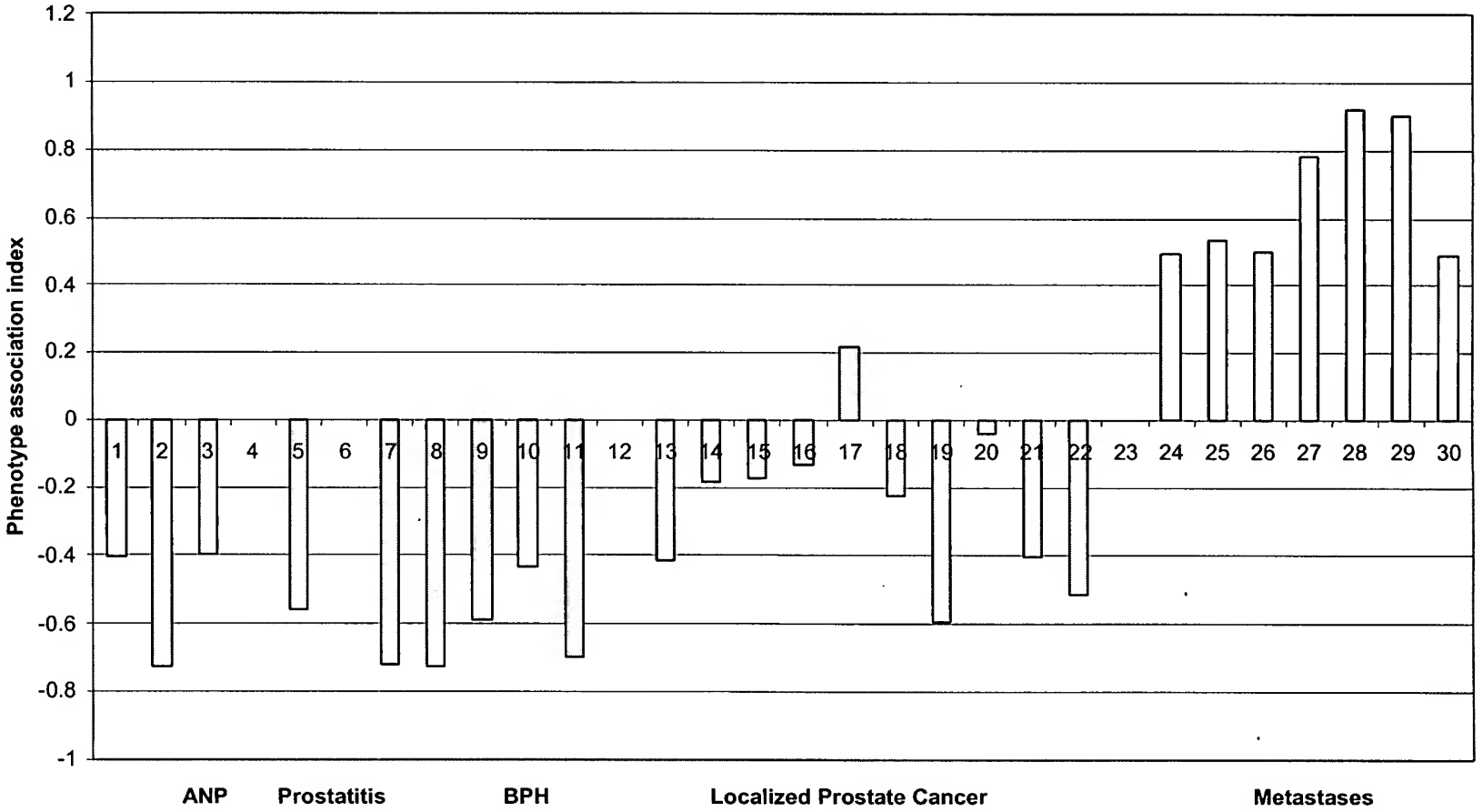


Figure 32. Phenotype association indices for 17 genes of metastasis seggregation class in 14 BPH samples, 4 ANP samples, prostatitis, 14 samples of localized prostate cancer (LPC), and 20 samples of metastatic prostate cancer (MPC).

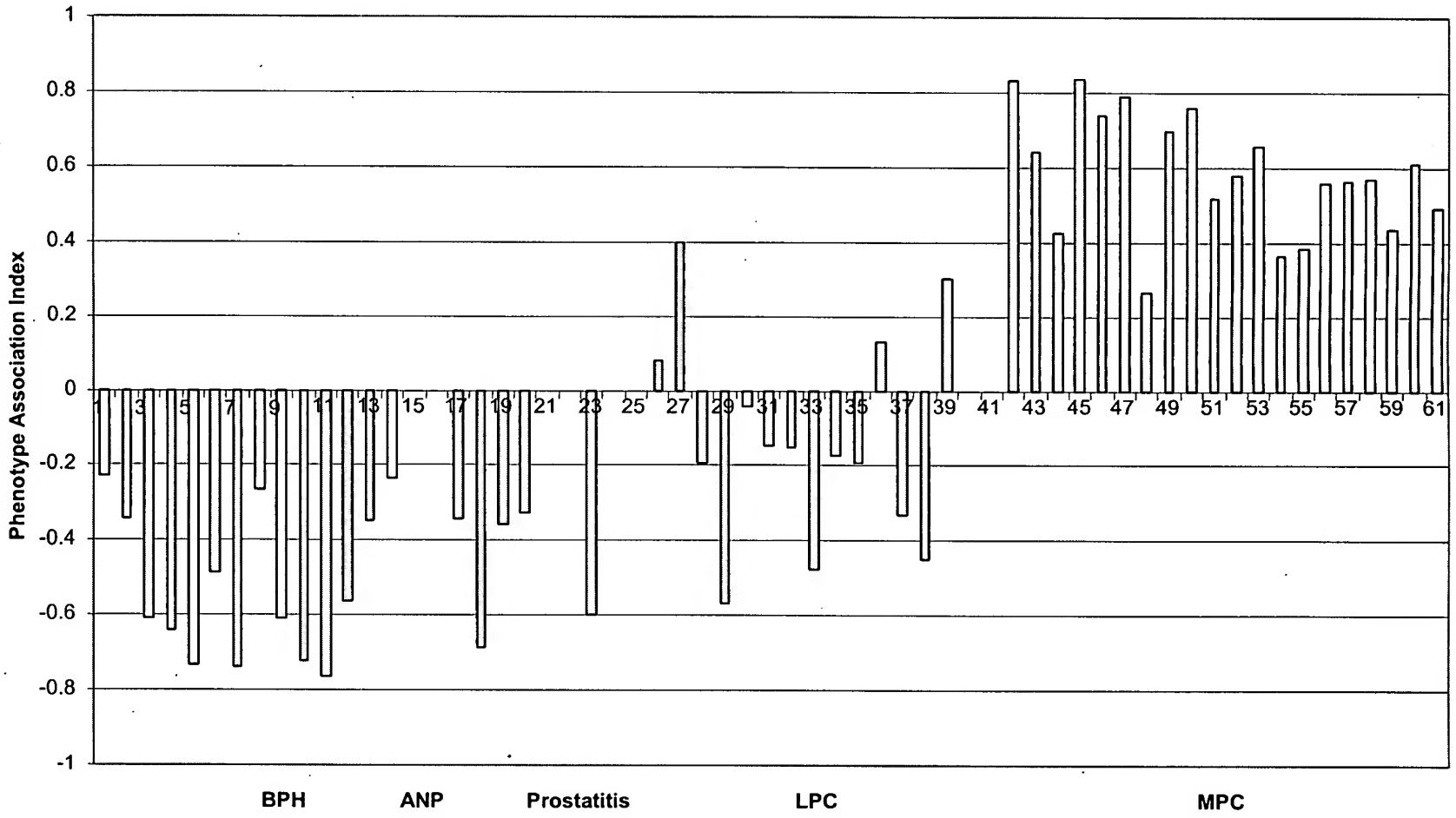


Figure 33. Phenotype association indices for 19 genes of metastasis seggregation class 2 in 14 BPH samples, 4 ANP samples, prostatitis, 14 samples of localized prostate cancer (LPC), and 20 samples of metastatic prostate cancer (MPC).

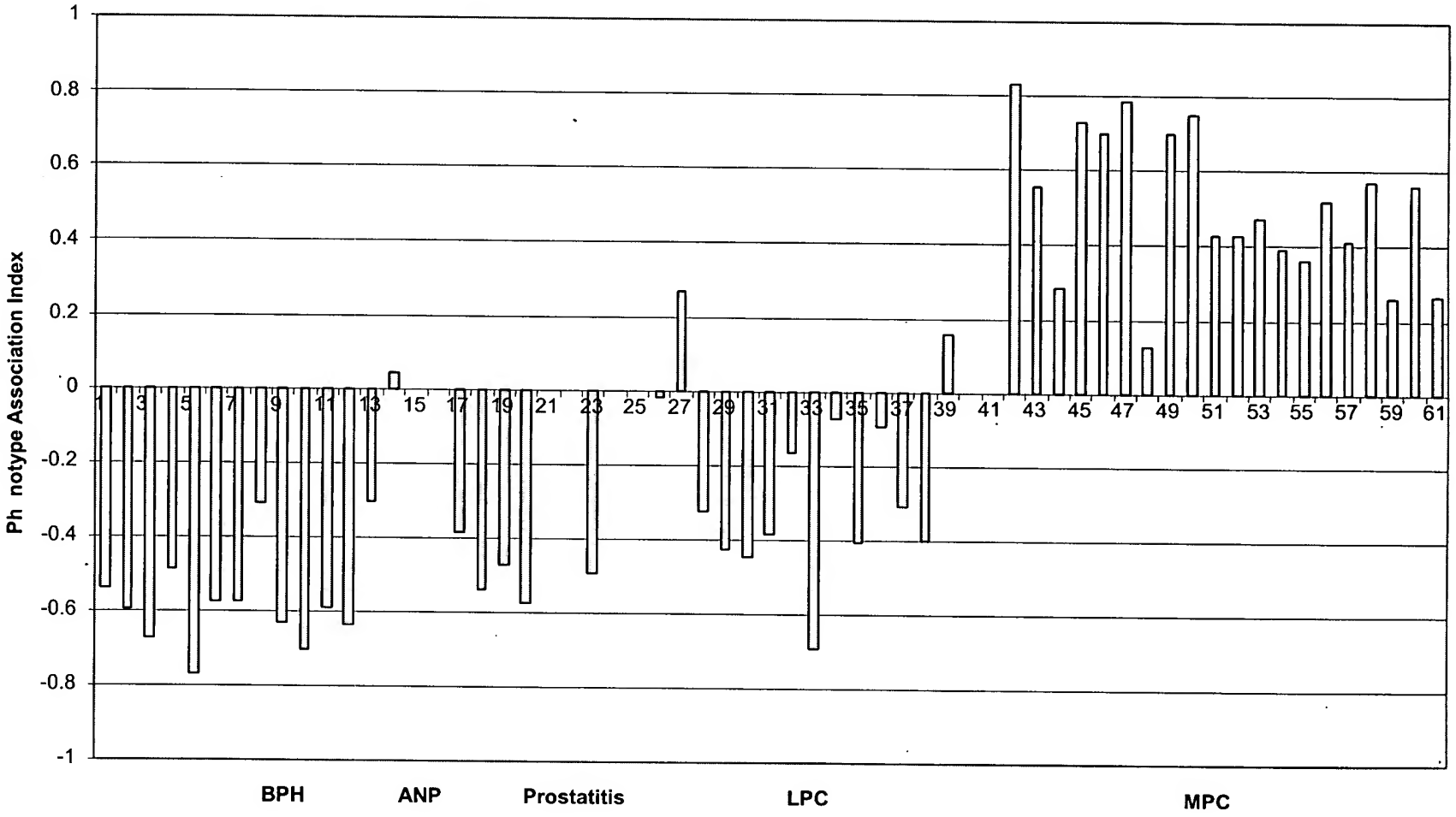


Figure 34. Phenotype association indices for 6 genes of the Q-PCR-based poor prognosis predictor class in 34 breast cancer patients who developed distant metastases within 5 years of diagnosis and 44 patients who continued to be disease-free

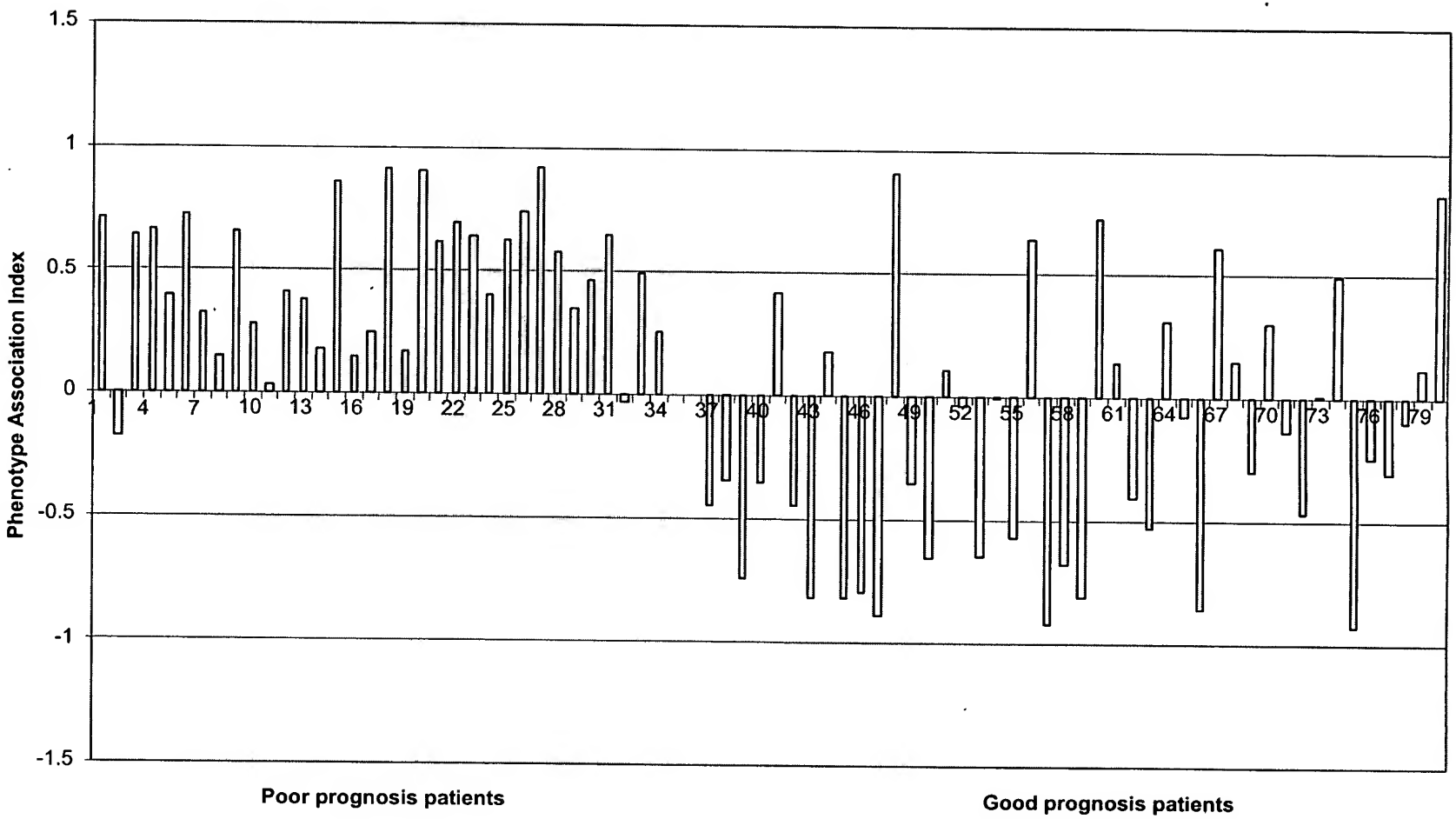


Figure 35. Phenotype association indexes for 14 genes of the Q-PCR-based good prognosis predictor class in 34 breast cancer patients who developed distant metastases within 5 years of diagnosis and 44 patients who continued to be disease-free

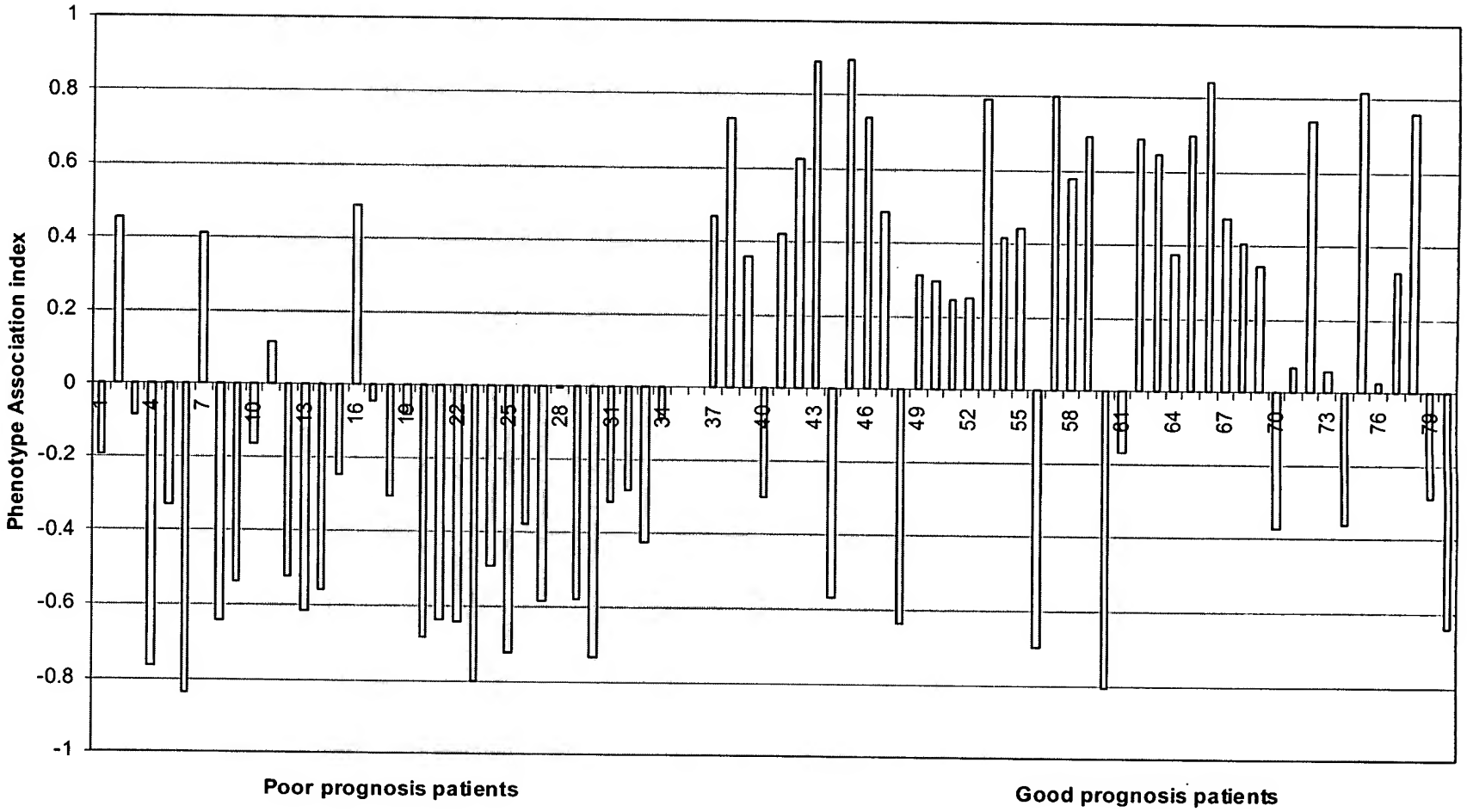


Figure 36. Phenotype association indices for 13 genes of the Q-PCR-based good prognosis predictor class in 34 breast cancer patients who developed distant metastases within 5 years of diagnosis and 44 patients who continued to be disease-free

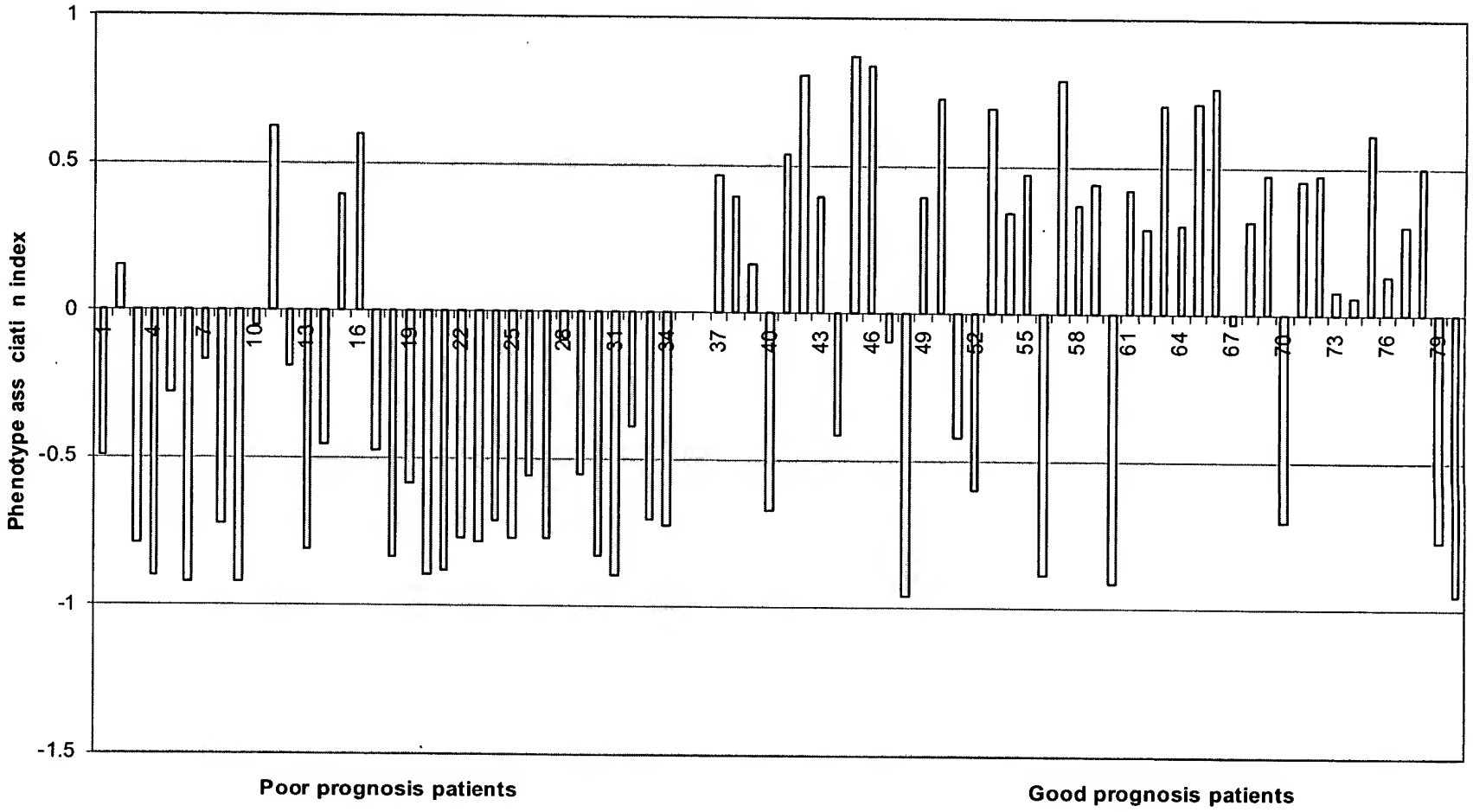


Figure 37. Phenotype association indices for 13 genes of the Q-PCR-based good prognosis predictor class in 11 breast cancer patients who developed distant metastases within 5 years of diagnosis and 8 patients who continued to be disease-free

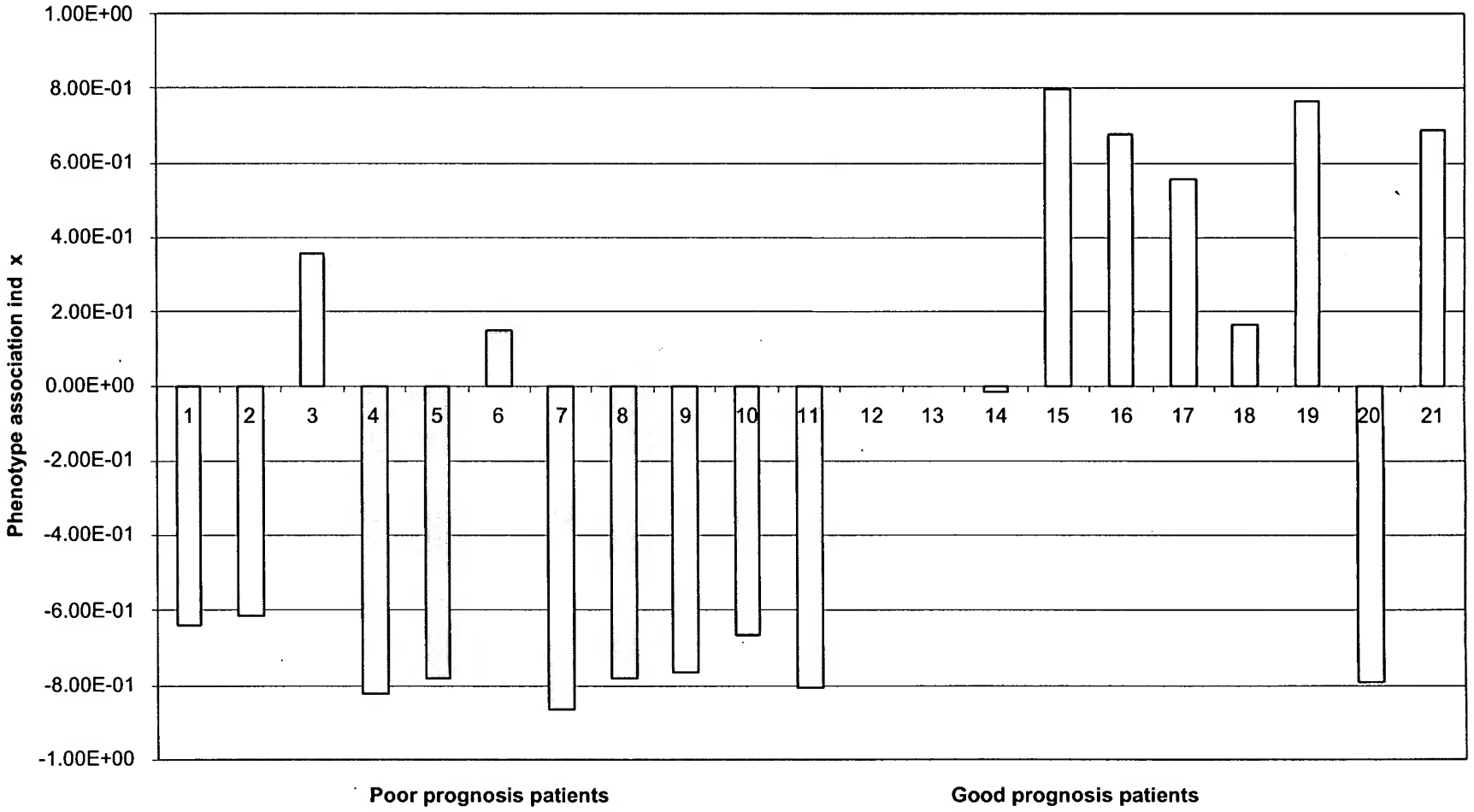


Figure 38. Phenotype association indices for 11 genes of the ovarian cancer poor prognosis predictor class in 11 tumors of well and moderate differention and 3 tumors of poor differentiation

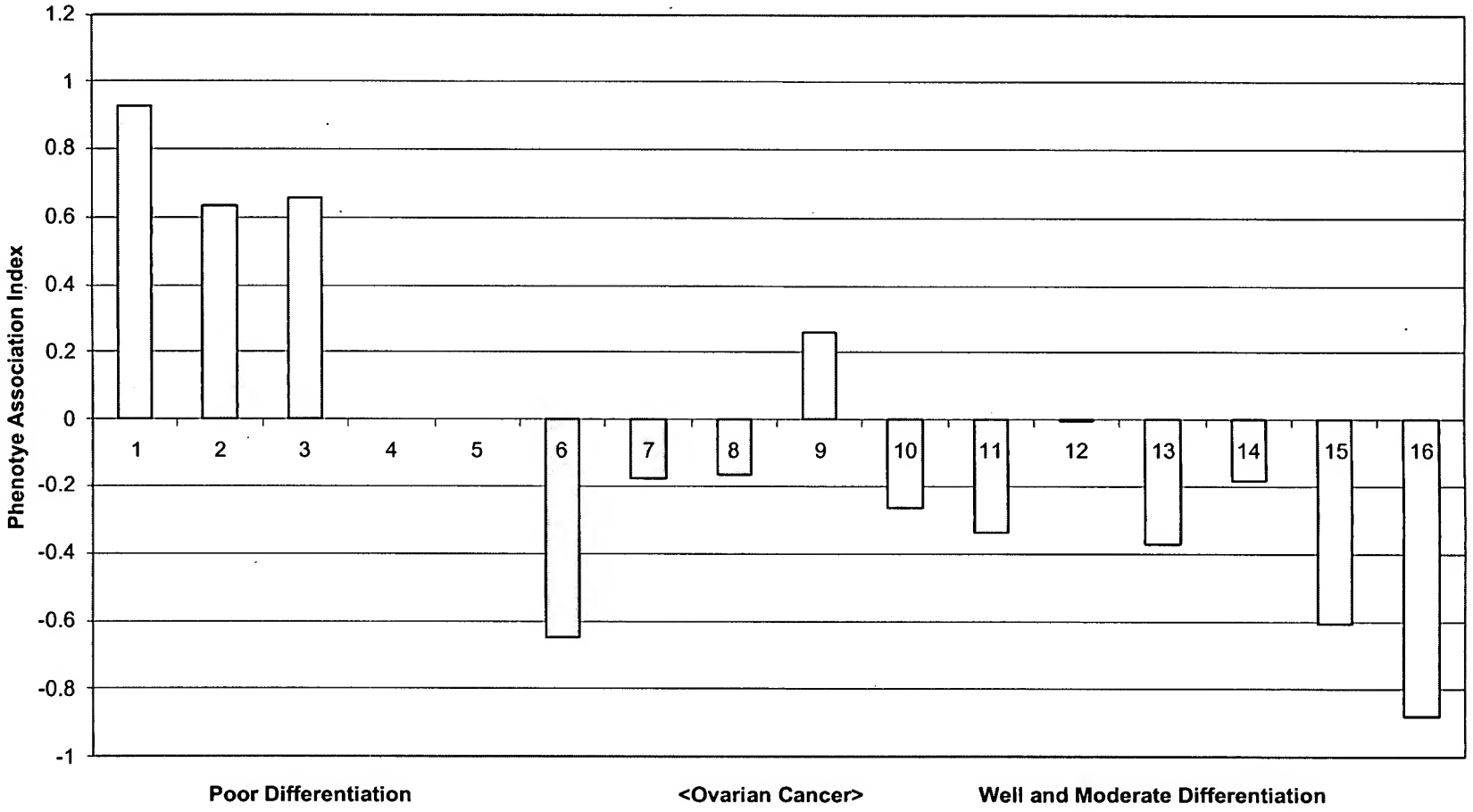


Figure 39. Phenotype association indices for 10 genes of the ovarian cancer good prognosis predictor class in 11 tumors of well and moderate differention and 3 tumors of poor differentiation

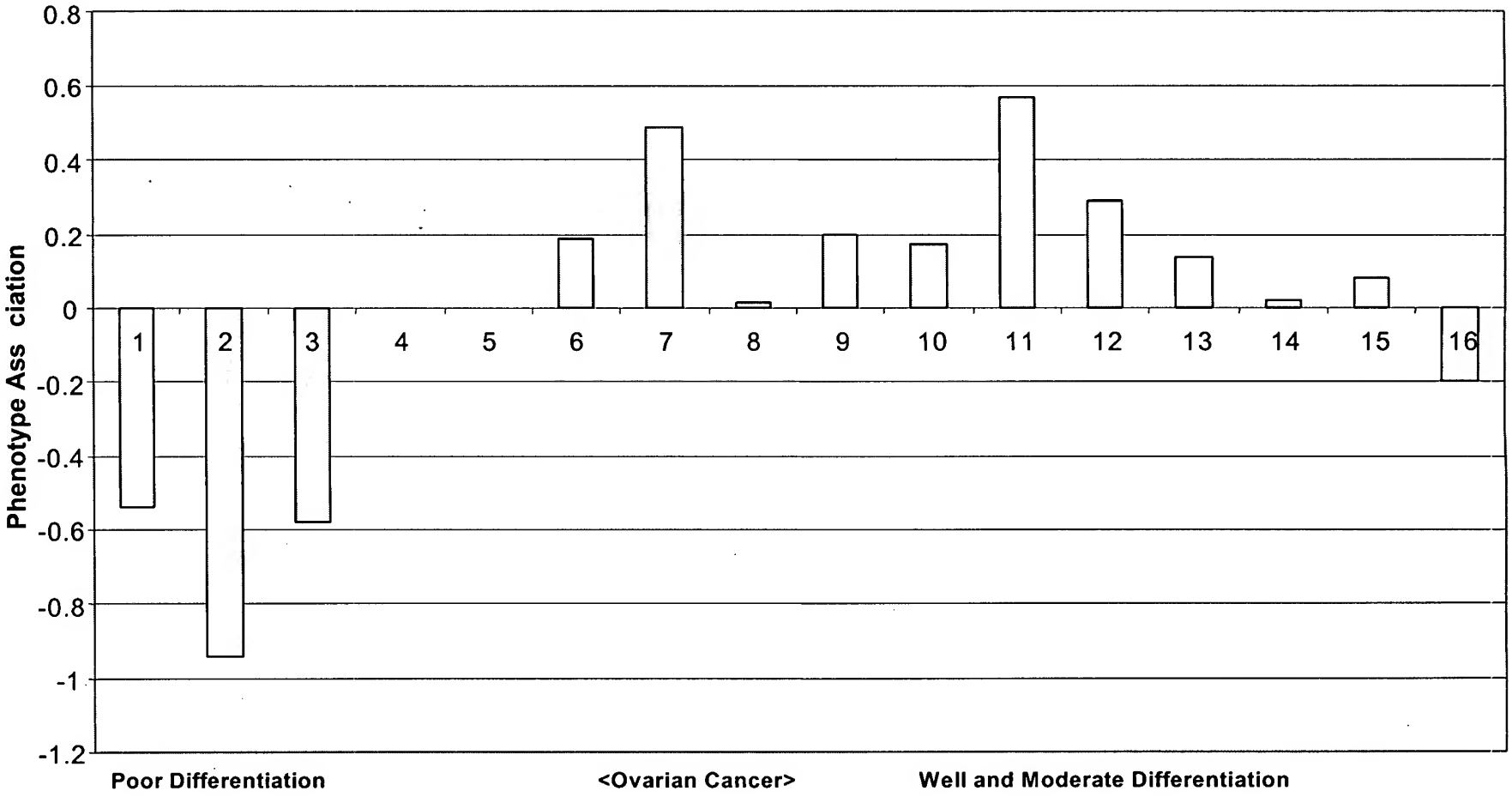


Figure 40. Correlation of the expression profiles in NSCLC cell lines versus normal bronchial epithelial cells and 139 adenocarcinoma samples versus 17 normal lung specimens for 13 genes of the human lung adenocarcinoma minimum seggregation cluster 1

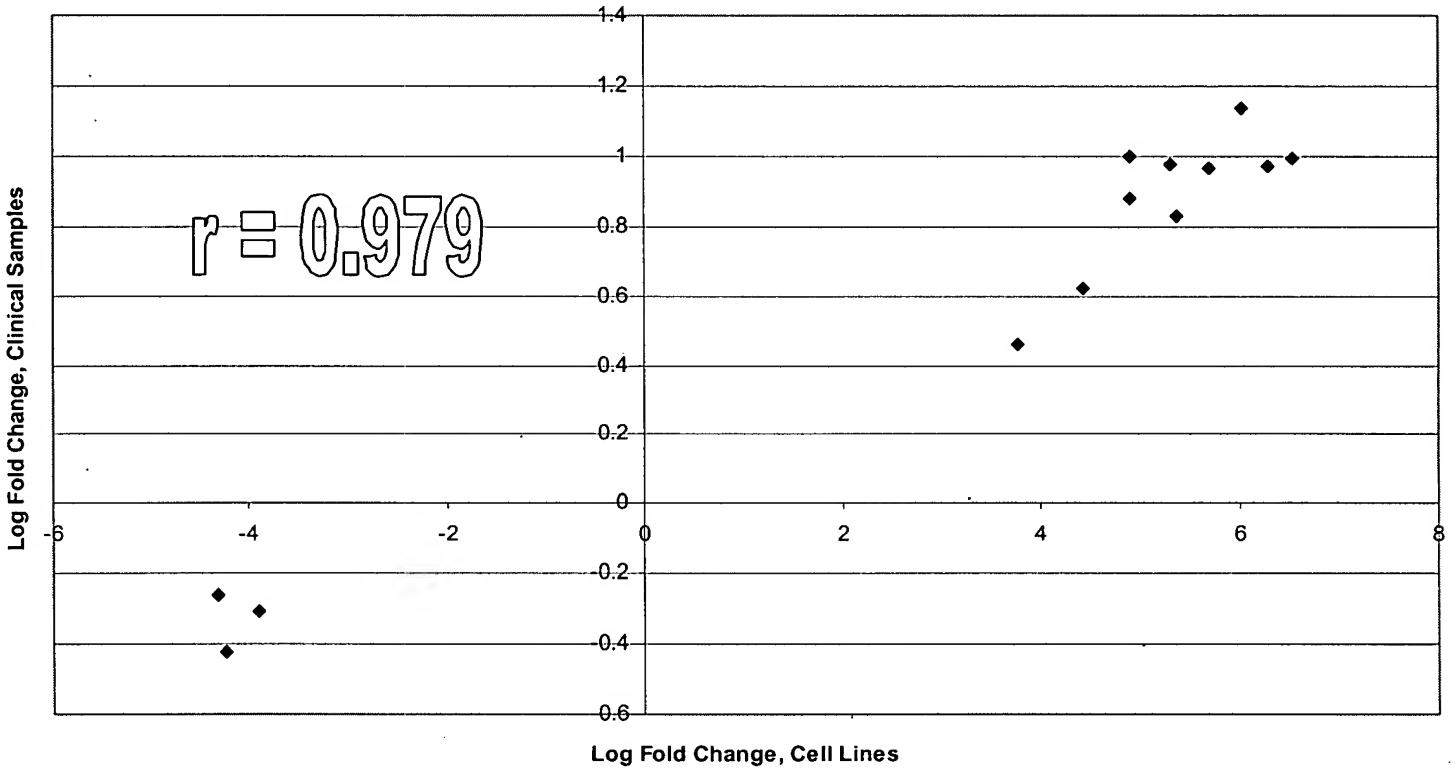


Figure 41. Correlation of the expression profiles in NSCLC cell lines versus normal bronchial epithelial cells and 139 adenocarcinoma samples versus 17 normal lung specimens for 26 genes of the human lung adenocarcinoma minimum seggregation cluster 2

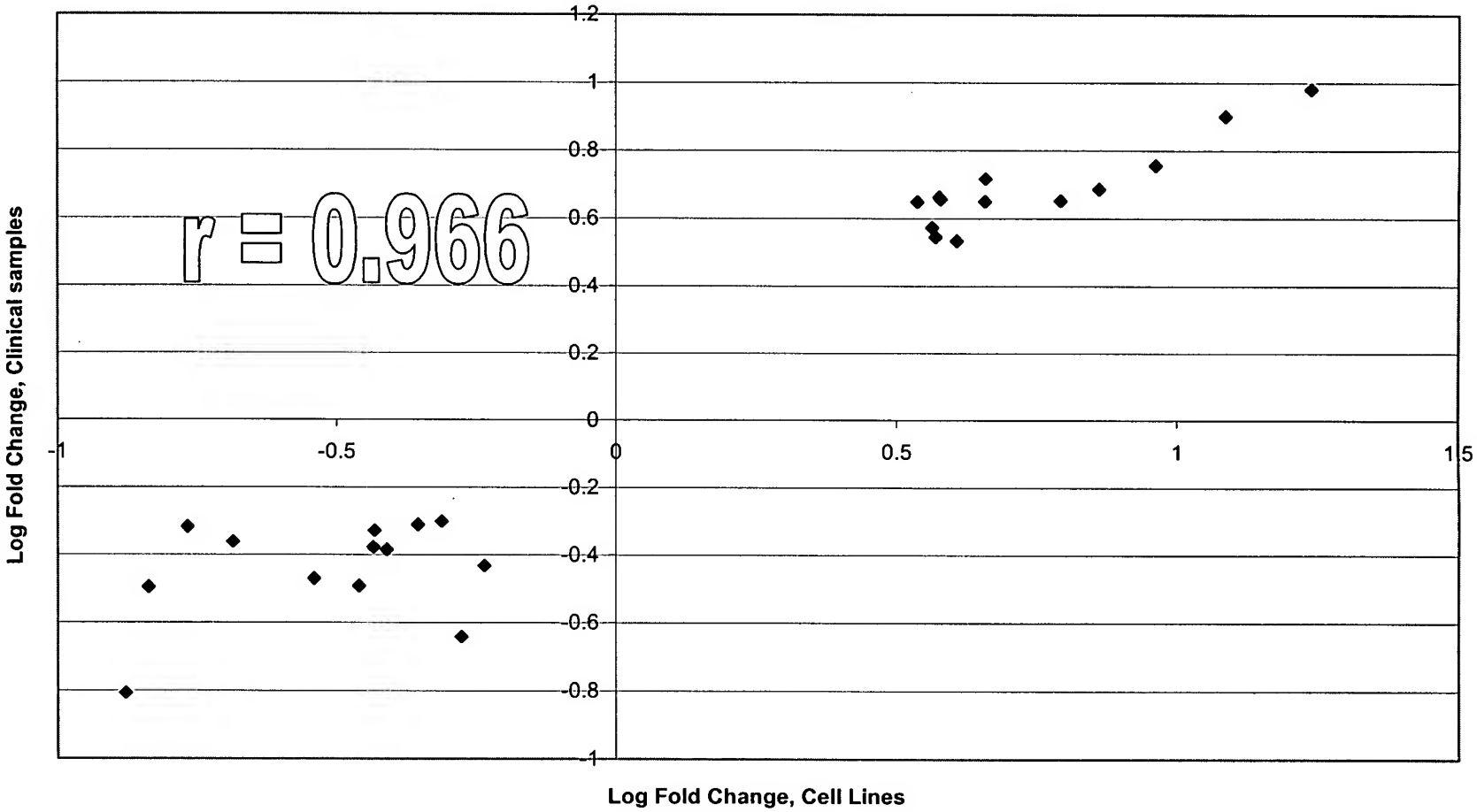


Figure 42. Phenotype association indices for 13 genes of the lung adenocarcinoma cluster 1 in 17 normal lung specimens and 139 lung adenocarcinoma samples

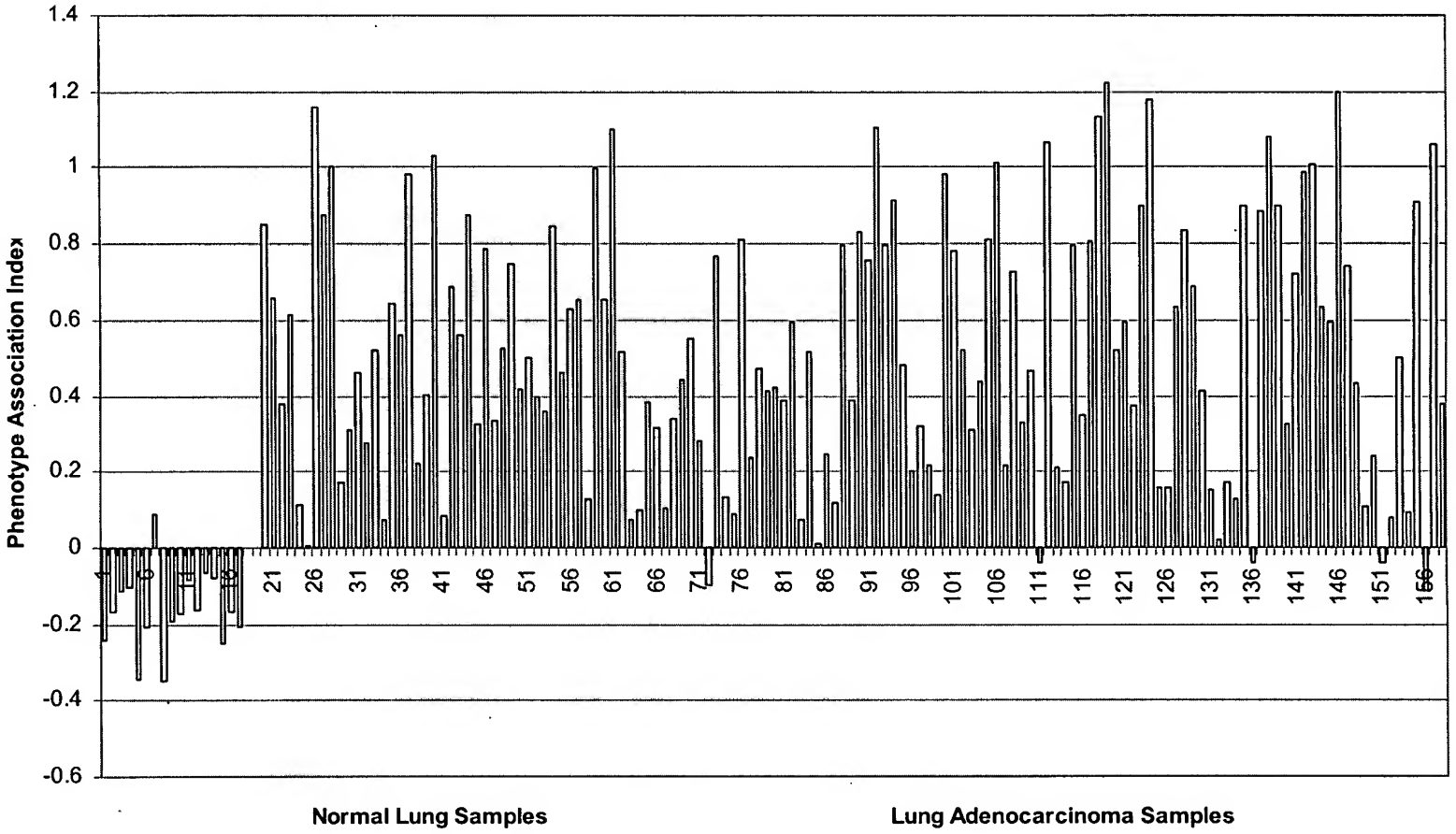


Figure 43. Phenotype association indices for 26 genes of the lung adenocarcinoma cluster 2 in 17 normal lung specimens and 139 lung adenocarcinoma samples

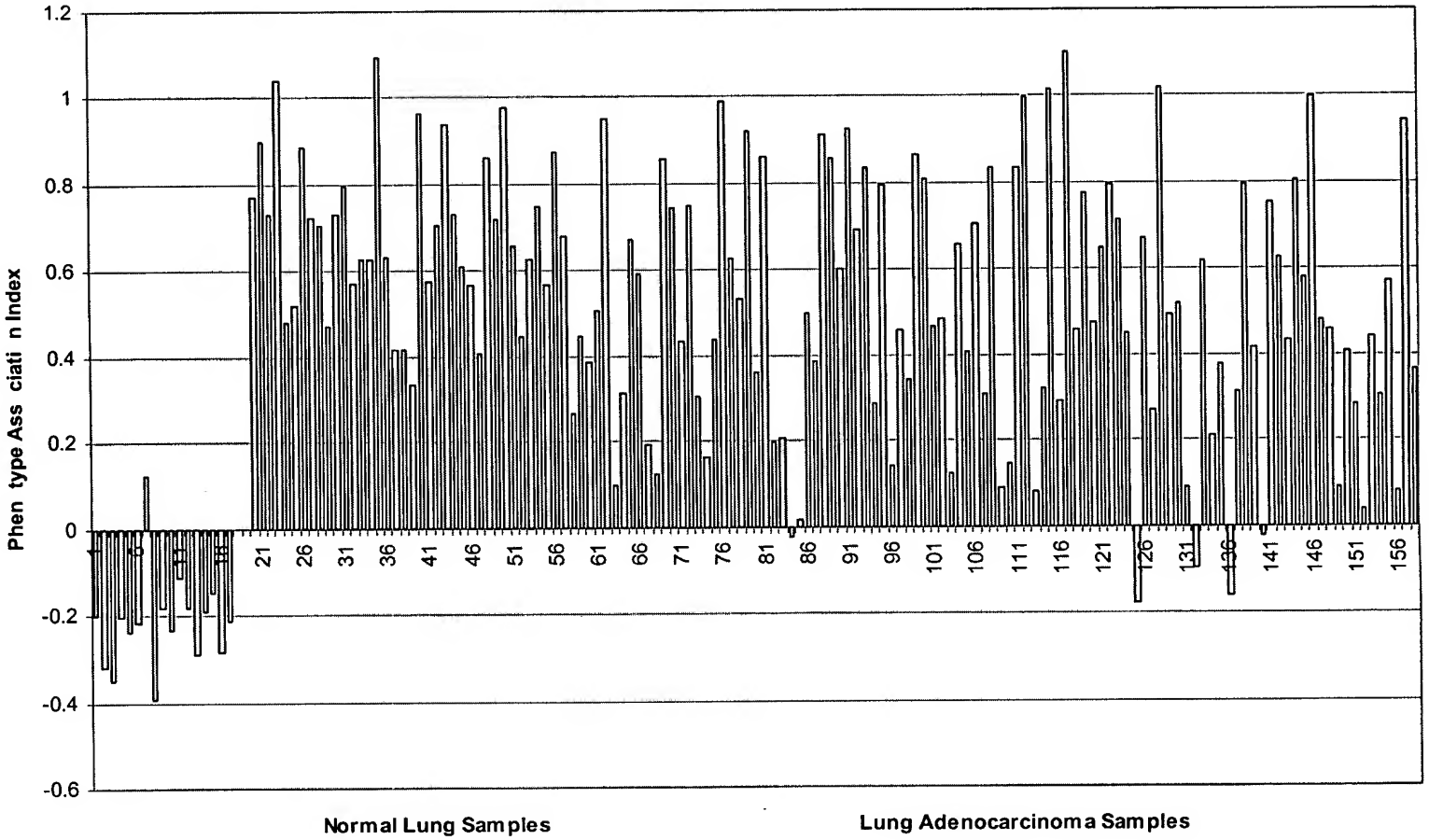


Figure 44. Correlation of the expression profiles in NSCLC cell lines versus normal bronchial epithelial cells and 34 NSCLC patients with poor prognosis versus 16 patients with good prognosis for 38 genes of lung adenocarcinoma poor prognosis cluster 1

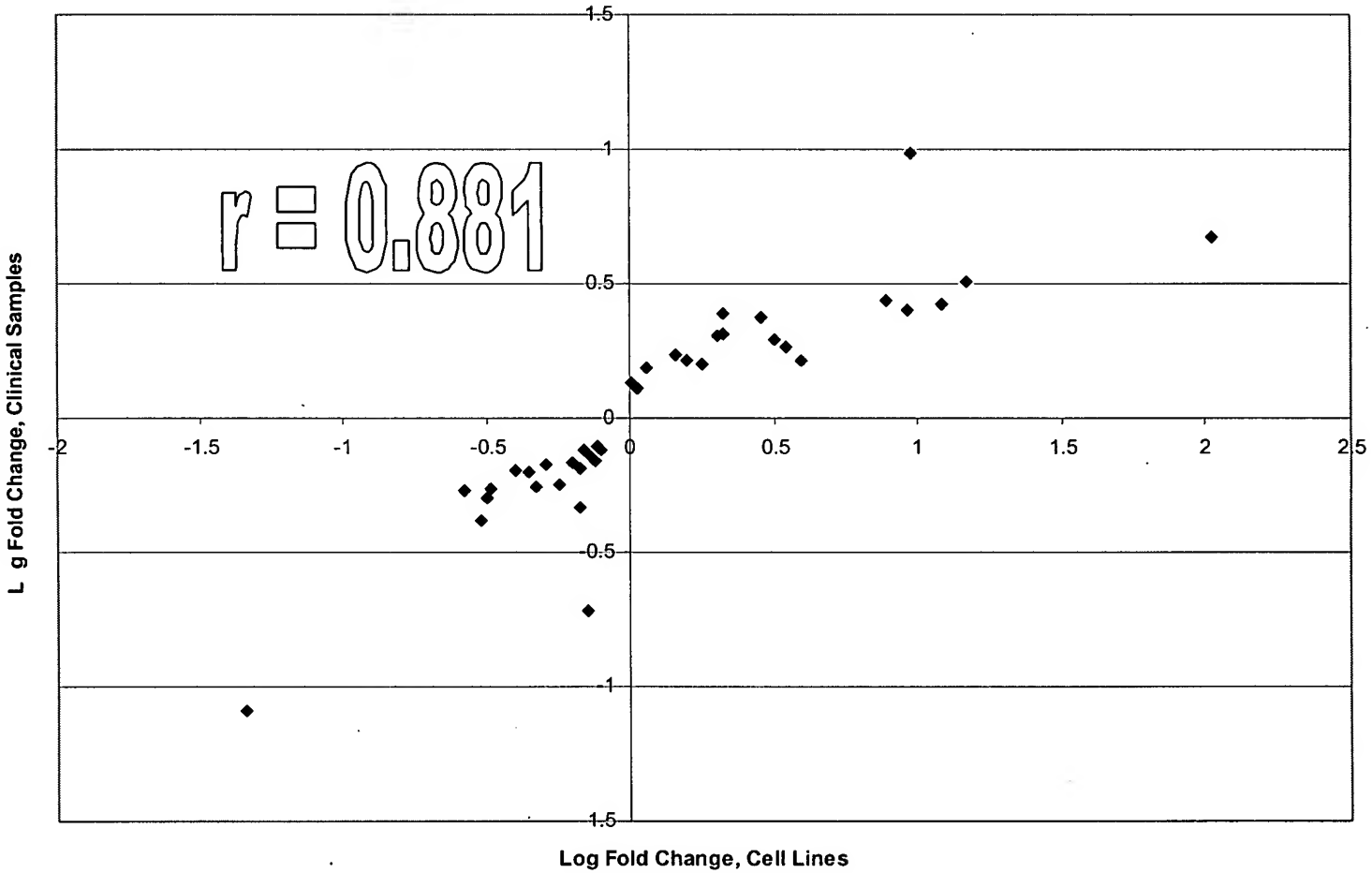
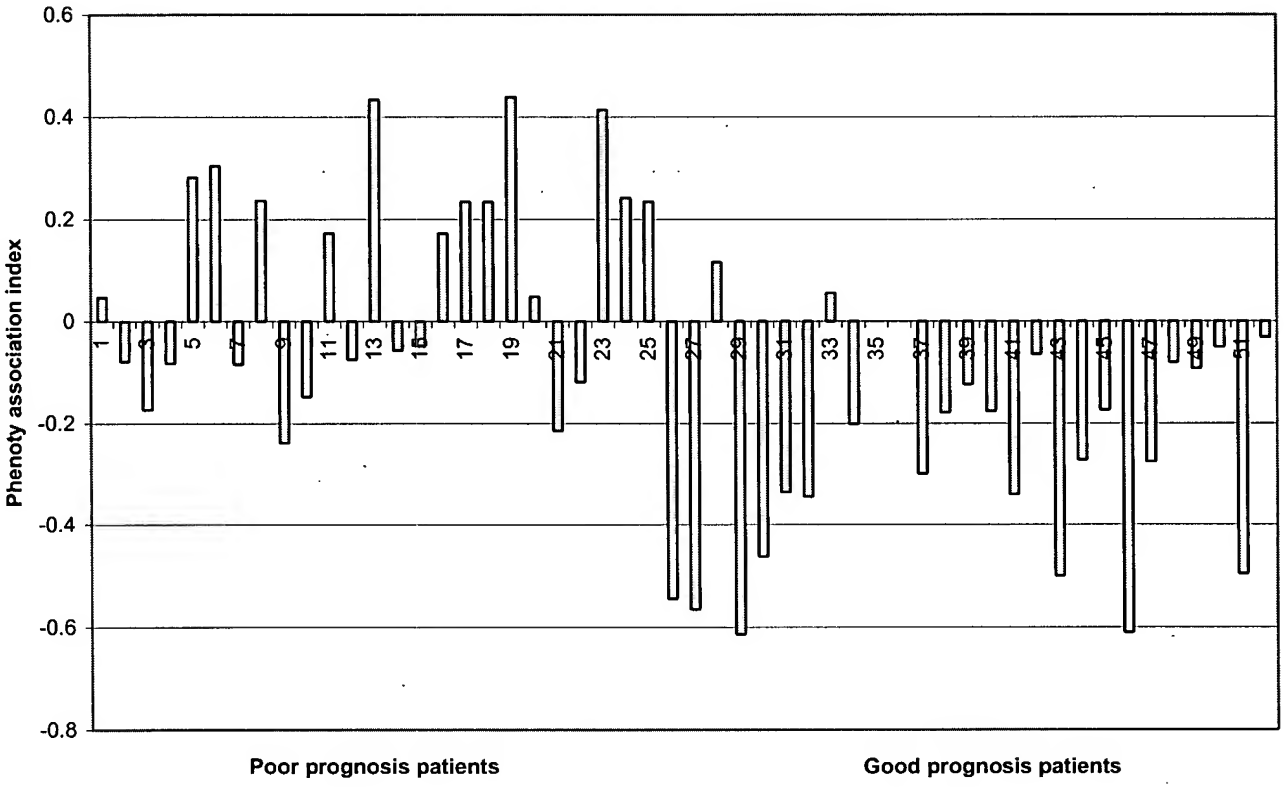
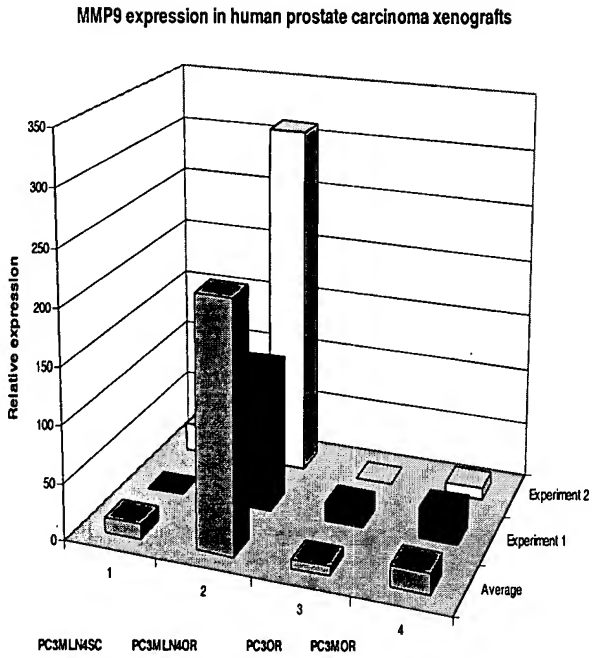


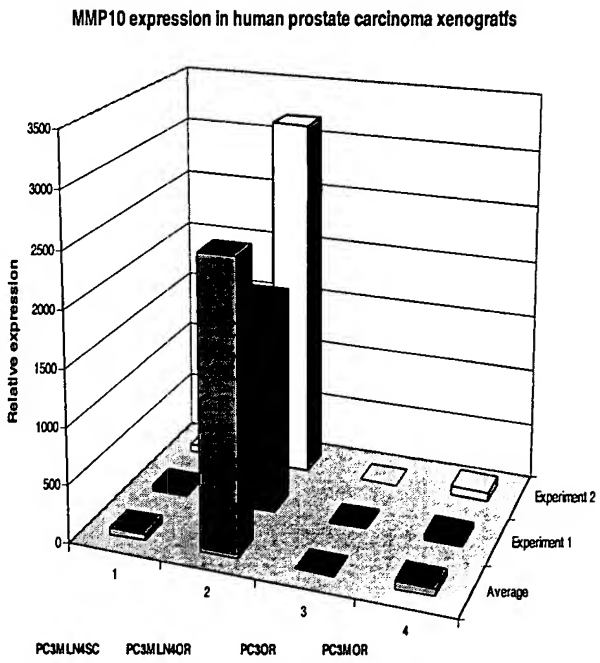
Figure 45. Phenotype association indices for 38 genes of the lung adenocarcinoma poor prognosis predictor cluster 1 in 34 NSCLC patients with poor prognosis and 16 patients with good prognosis



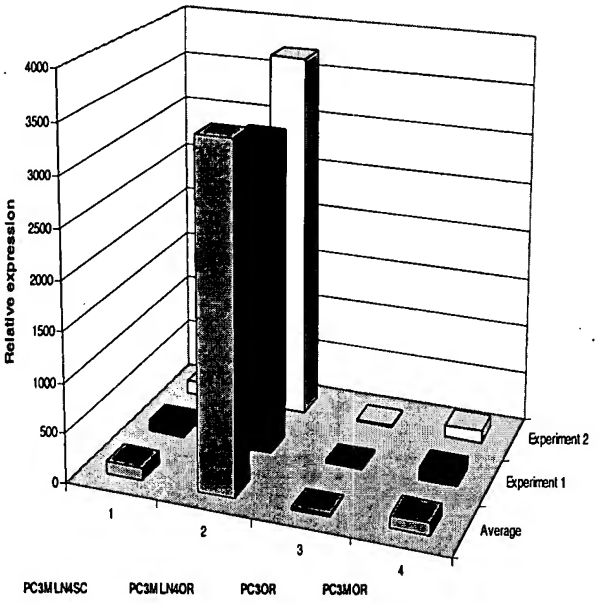
A1


MMP9 expression in human prostate carcinoma xenografts
Relative expression
350
300
250
200
150
100
50
0
1
2
3
4
Experiment 2
Experiment 1
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3M OR

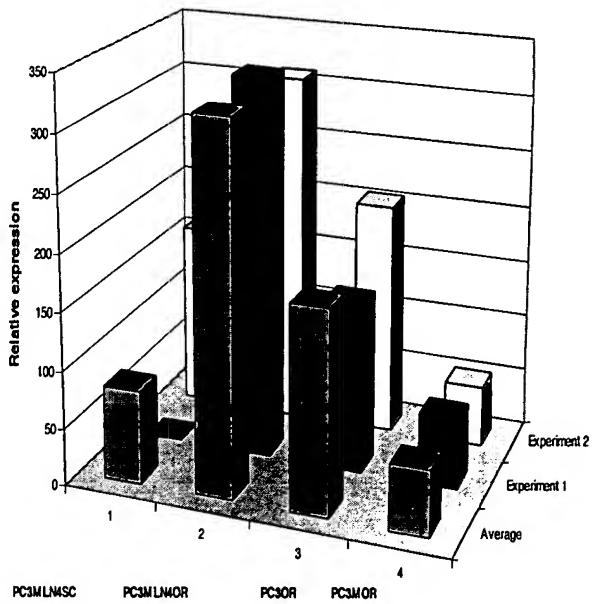
A2.


MMP10 expression in human prostate carcinoma xenografts
Relative expression
3500
3000
2500
2000
1500
1000
500
0
1
2
3
4
Experiment 2
Experiment 1
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3M OR

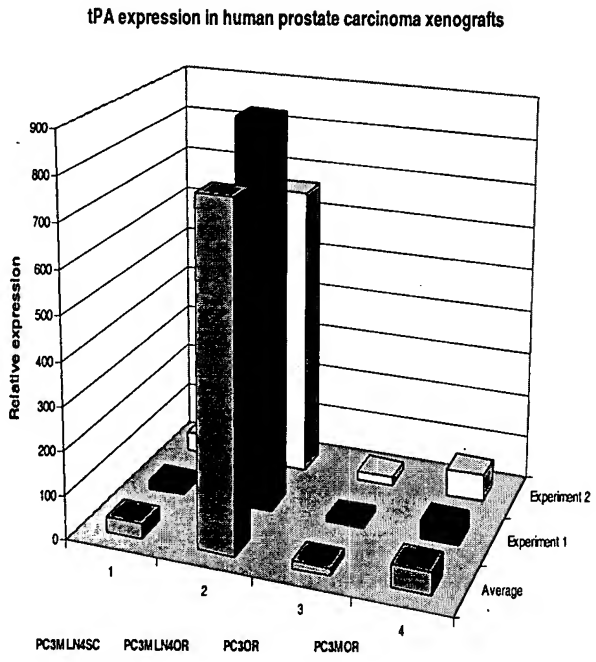
A3


MMP1 expression in human prostate carcinoma xenografts
Relative expression
4000
3500
3000
2500
2000
1500
1000
500
0
1
2
3
4
Experiment 2
Experiment 1
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3M OR

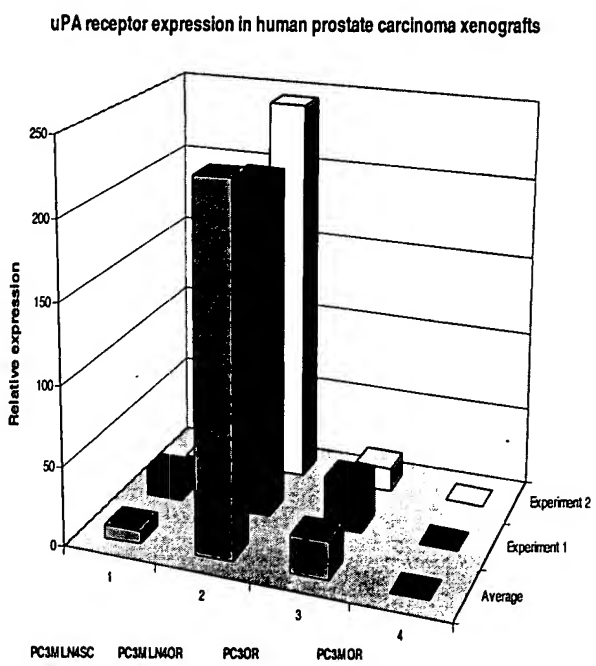
A4.


MMP14 expression in human prostate carcinoma xenografts
Relative expression
350
300
250
200
150
100
50
0
1
2
3
4
Experiment 2
Experiment 1
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3M OR

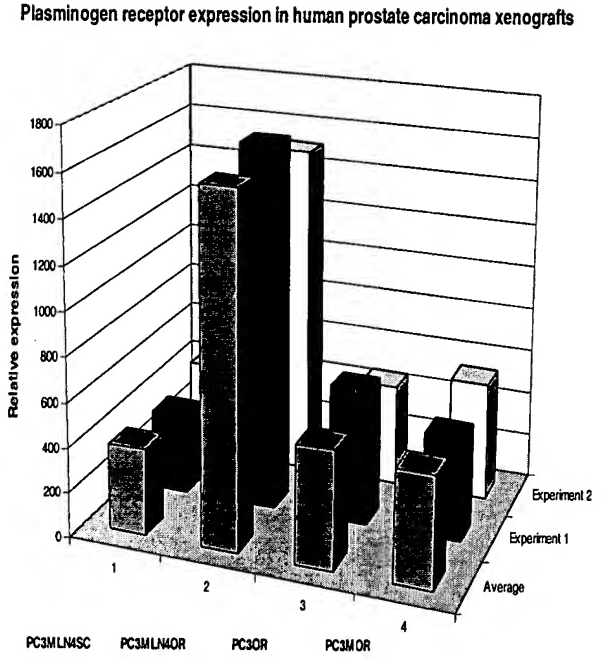
B1


tPA expression in human prostate carcinoma xenografts
Relative expression
900
800
700
600
500
400
300
200
100
0
1
2
3
4
Experiment 2
Experiment 1
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3M OR

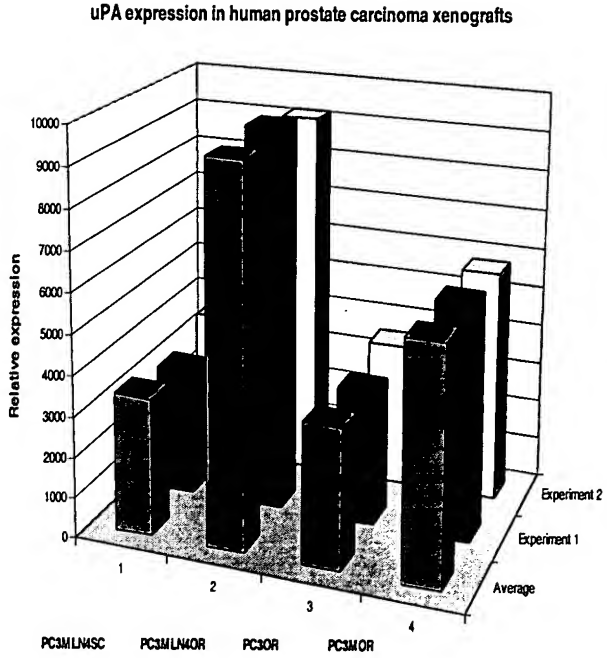
B2.


uPA receptor expression in human prostate carcinoma xenografts
Relative expression
250
200
150
100
50
0
1
2
3
4
Experiment 2
Experiment 1
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3M OR

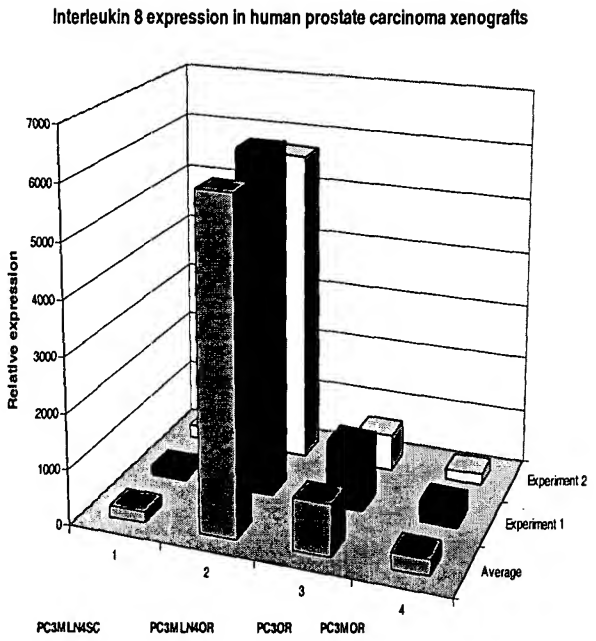
B3


Plasminogen receptor expression in human prostate carcinoma xenografts
Relative expression
1800
1600
1400
1200
1000
800
600
400
200
0
1
2
3
4
Experiment 2
Experiment 1
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3M OR

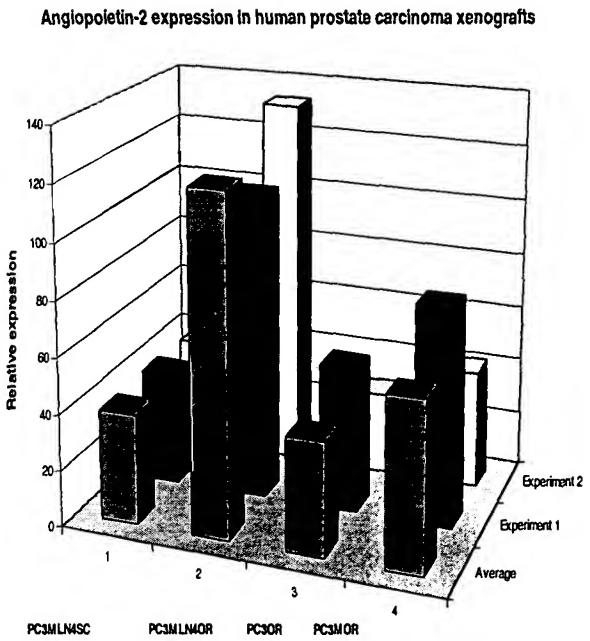
B4.


uPA expression in human prostate carcinoma xenografts
Relative expression
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
1
2
3
4
Experiment 2
Experiment 1
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3M OR

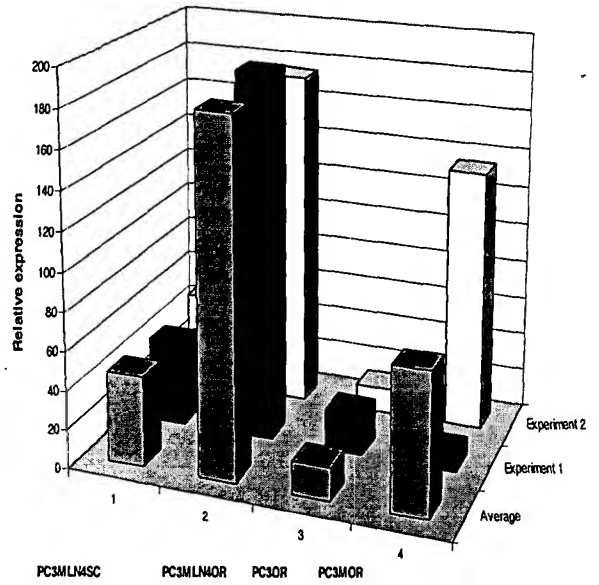
C1


Interleukin 8 expression in human prostate carcinoma xenografts
Relative expression
7000
6000
5000
4000
3000
2000
1000
0
Experiment 2
Experiment 1
Average
1
2
3
4
PC3MLN4SC
PC3MLN4OR
PC3OR
PC3MOR

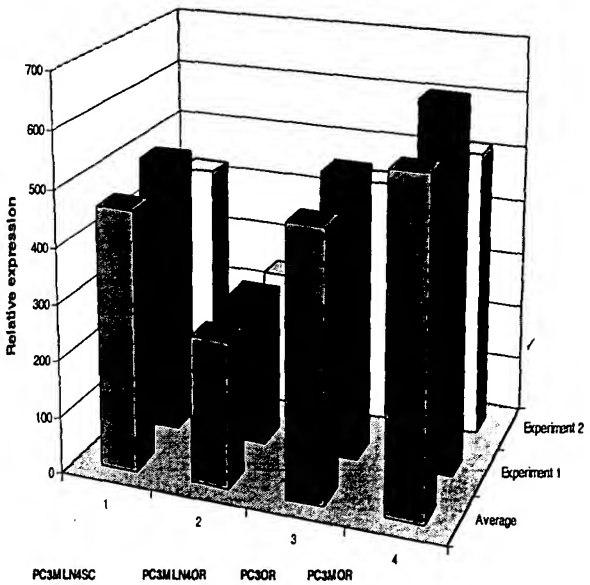
C2.


Angiopoietin-2 expression in human prostate carcinoma xenografts
Relative expression
140
120
100
80
60
40
20
0
Experiment 2
Experiment 1
Average
1
2
3
4
PC3MLN4SC
PC3MLN4OR
PC3OR
PC3MOR

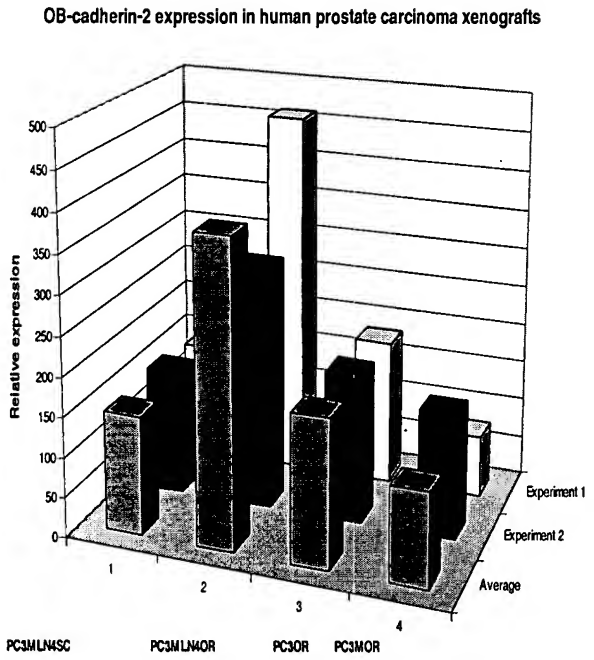
C3


Osteopontin expression in human prostate carcinoma xenografts
Relative expression
200
180
160
140
120
100
80
60
40
20
0
Experiment 2
Experiment 1
Average
1
2
3
4
PC3MLN4SC
PC3MLN4OR
PC3OR
PC3MOR

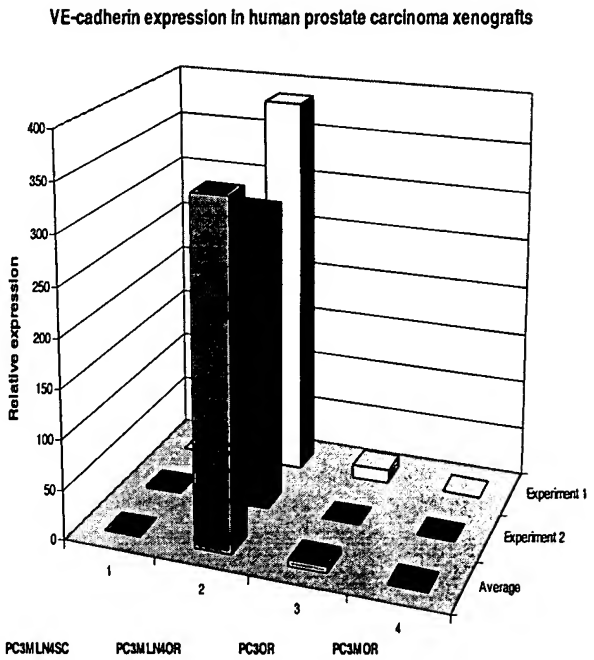
C4.


Maspin expression in human prostate carcinoma xenografts
Relative expression
700
600
500
400
300
200
100
0
Experiment 2
Experiment 1
Average
1
2
3
4
PC3MLN4SC
PC3MLN4OR
PC3OR
PC3MOR

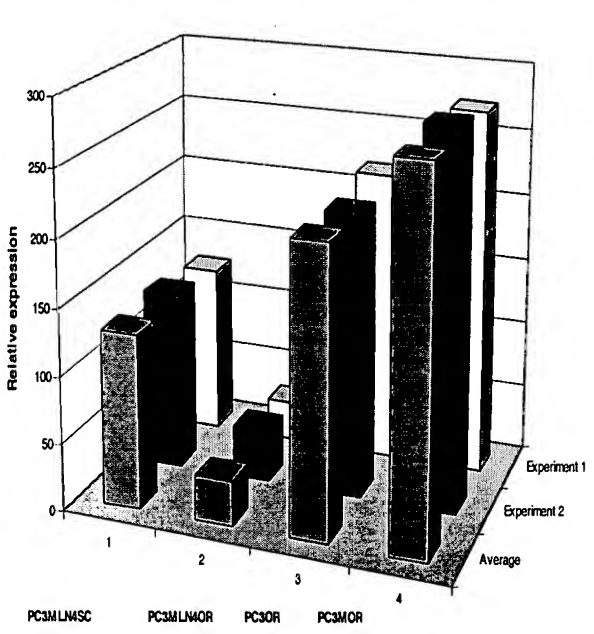
D1


OB-cadherin-2 expression in human prostate carcinoma xenografts
Relative expression
500
450
400
350
300
250
200
150
100
50
0
1
2
3
4
Experiment 1
Experiment 2
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3MOR

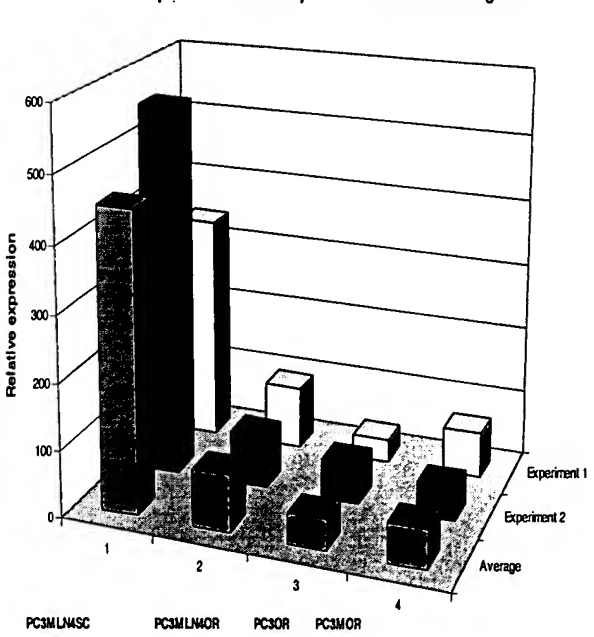
D2.


VE-cadherin expression in human prostate carcinoma xenografts
Relative expression
400
350
300
250
200
150
100
50
0
1
2
3
4
Experiment 1
Experiment 2
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3MOR

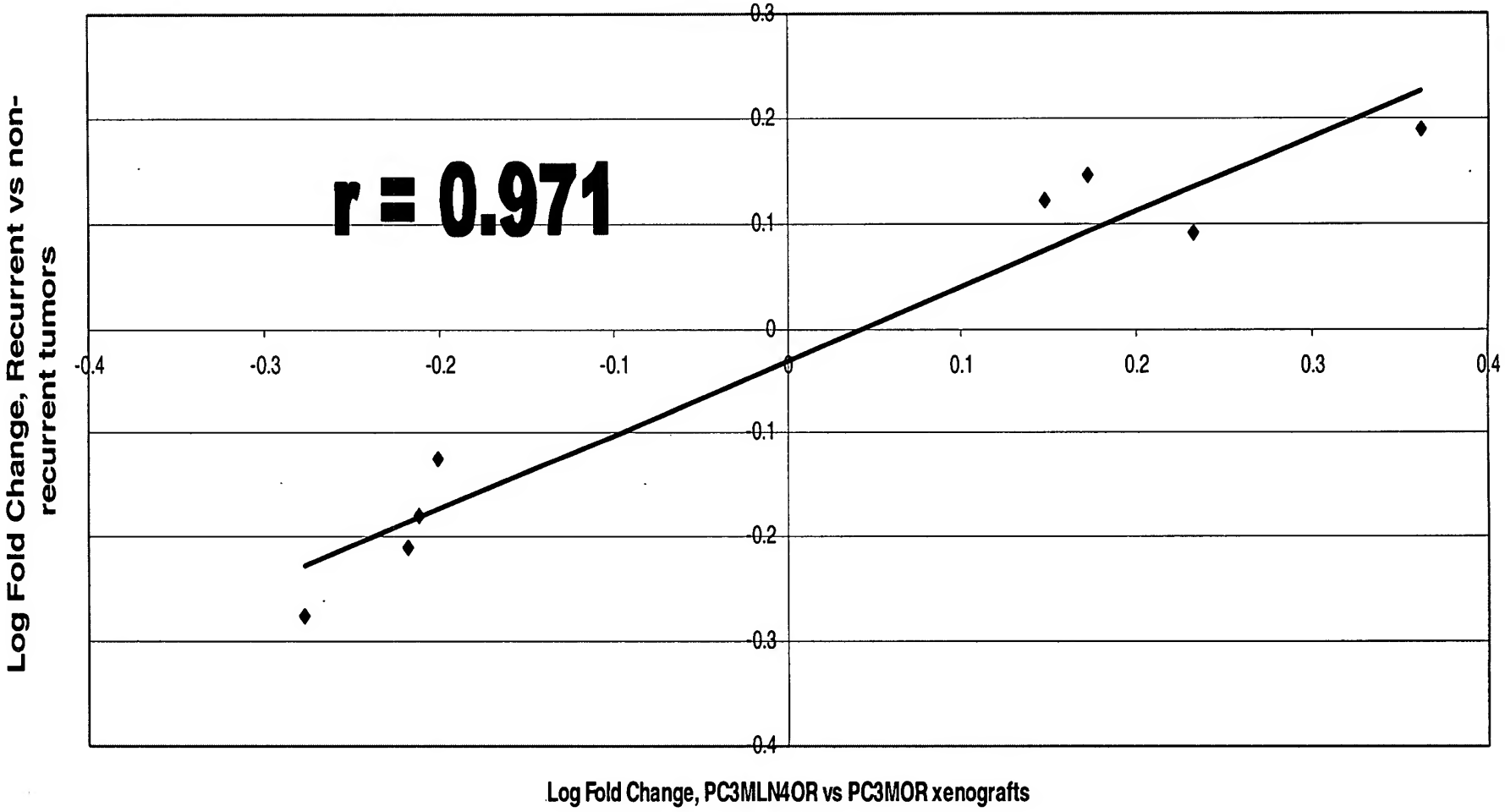
D3.


E-cadherin expression in human prostate carcinoma xenografts
Relative expression
300
250
200
150
100
50
0
1
2
3
4
Experiment 1
Experiment 2
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3MOR

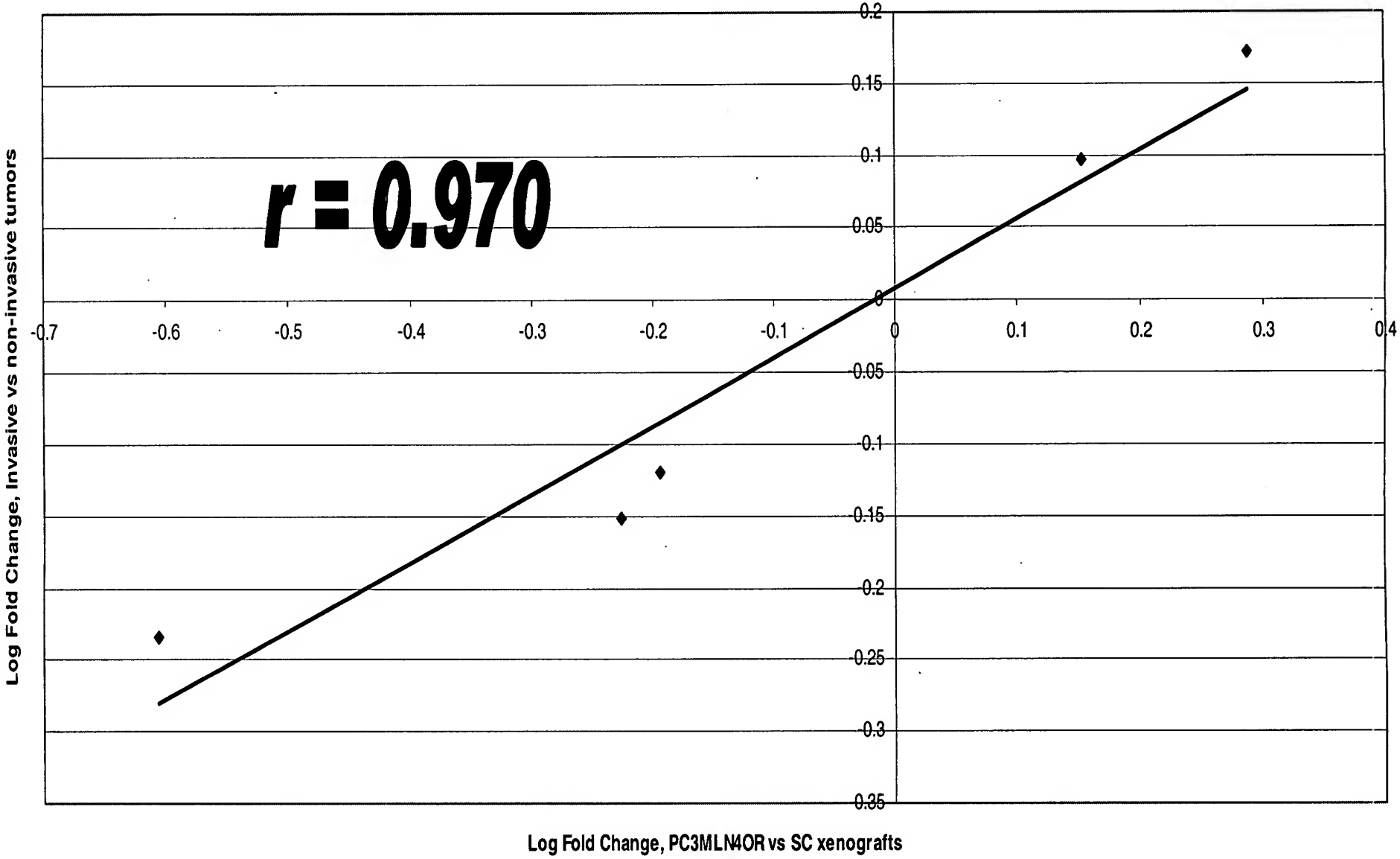
D4.


N-cadherin expression in human prostate carcinoma xenografts
Relative expression
600
500
400
300
200
100
0
1
2
3
4
Experiment 1
Experiment 2
Average
PC3M LN4SC
PC3M LN4OR
PC3OR
PC3MOR

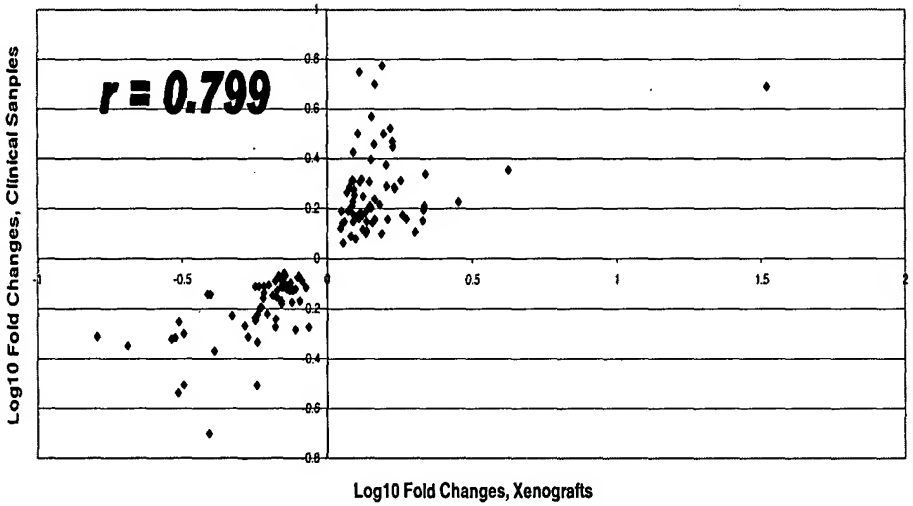
47A. Correlation of the expression profiles for 8 genes of the prostate cancer recurrence predictor class in orthotopic xenografts and 8 recurrent versus 13 non-recurrent human prostate tumors



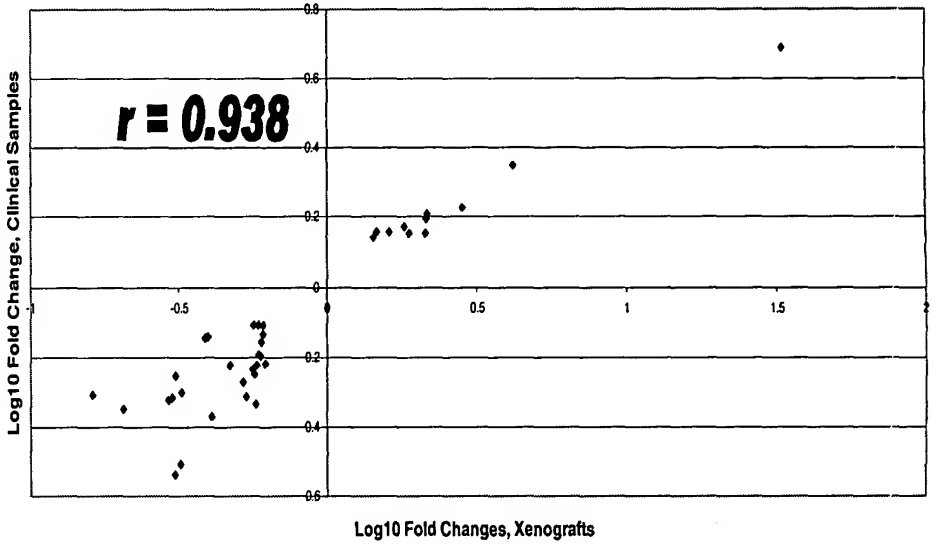
47B. Correlation of the expression profiles for 5 genes of the prostate cancer invasion predictor cluster in orthotopic xenografts and 26 invasive versus 26 non-invasive human prostate tumors



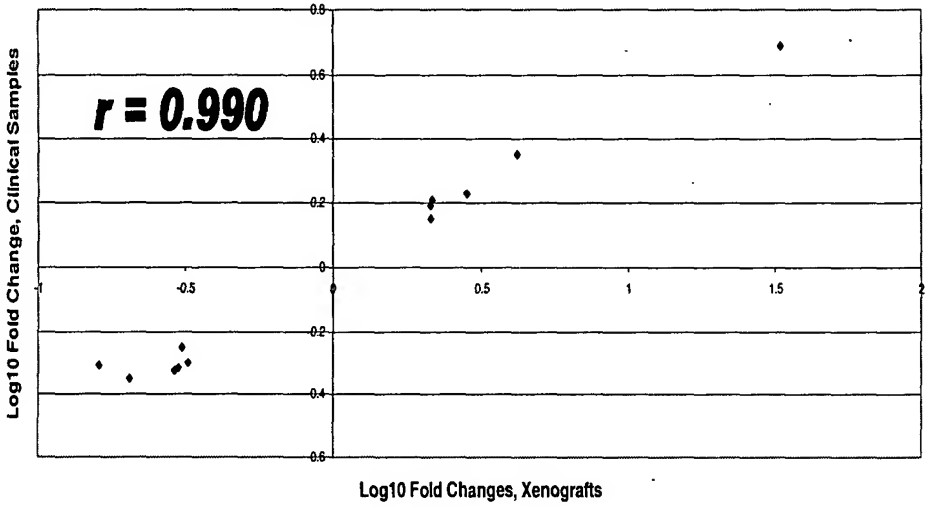
48A. Correlation of the expression profiles for 131 transcripts of the prostate cancer metastasis seggregation cluster in PC-3MLN4 orthotopic versus s.c. xenografts and metastatic versus primary human prostate tumors



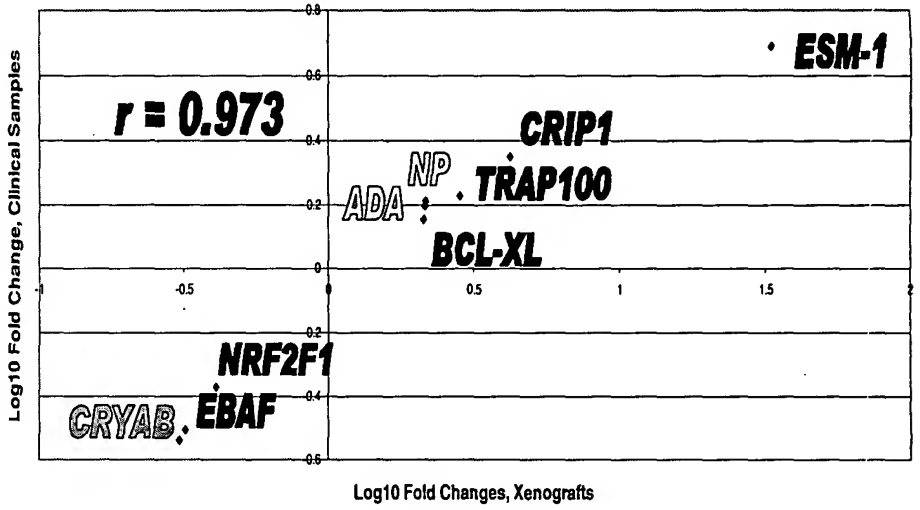
48B. Correlation of the expression profiles for 37 transcripts of the prostate cancer metastasis seggregation cluster in PC-3MLN4 orthotopic versus s.c. xenografts and metastatic versus primary human prostate tumors



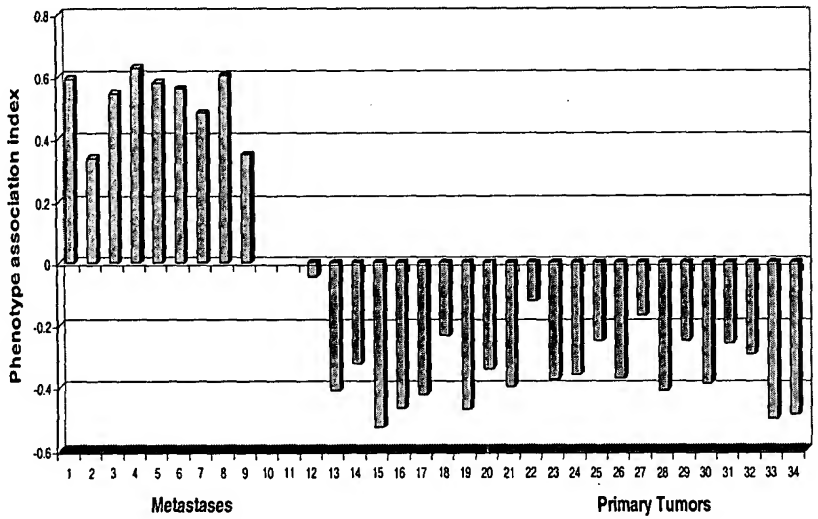
48C. Correlation of the expression profiles for 12 transcripts of the prostate cancer metastasis seggregation cluster in PC-3MLN4 orthotopic versus s.c. xenografts and metastatic versus primary human prostate tumors



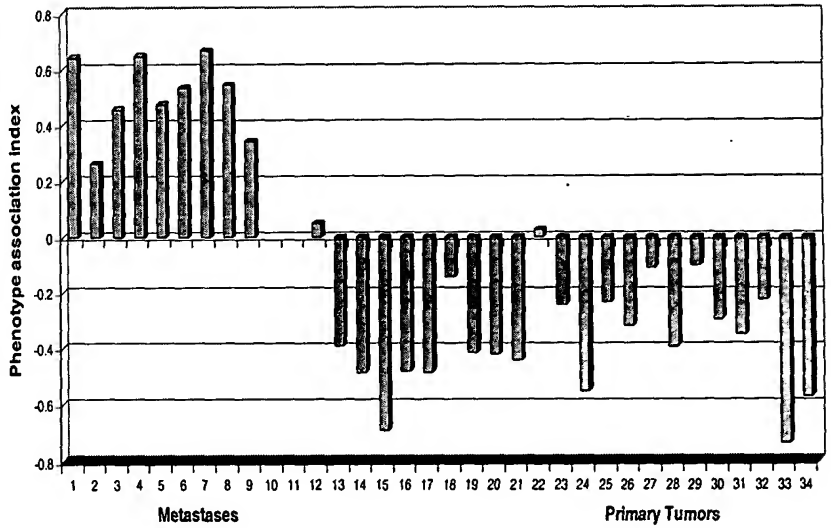
48D. Correlation of the expression profiles for 9 transcripts of the prostate cancer metastasis seggregation cluster in PC-3MLN4 orthotopic versus s.c. xenografts and metastatic versus primary human prostate tumors



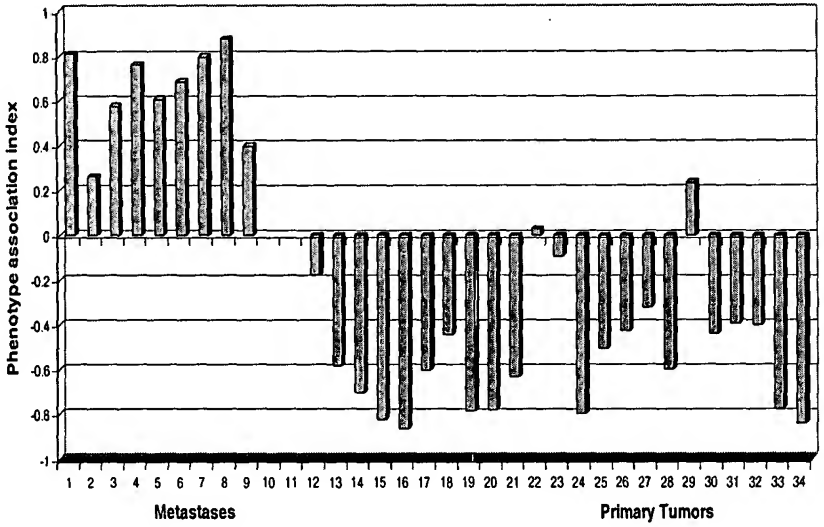
49A. Phenotype association indices of the 131 gene signature of the human prostate cancer metastasis in 9 metastatic and 23 primary human prostate tumors



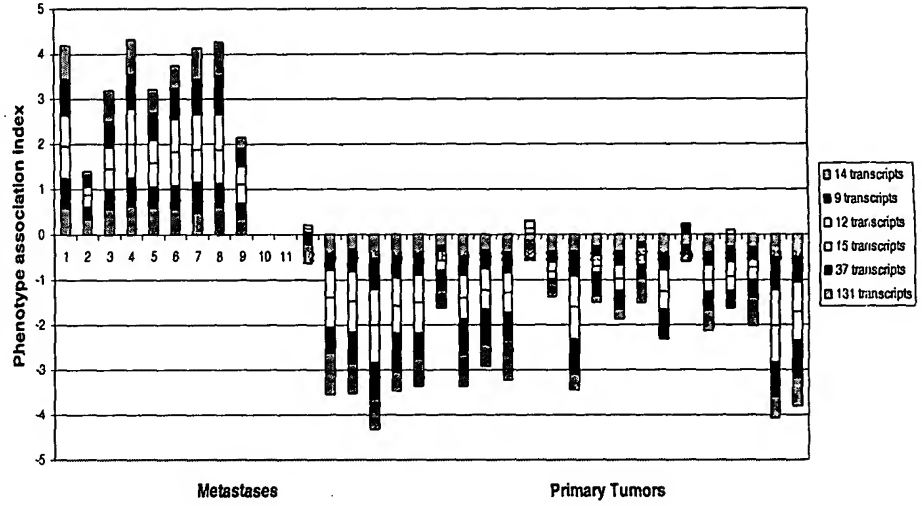
49B. Phenotype association indices of the 37 gene signature of the human prostate cancer metastasis in 9 metastatic and 23 primary human prostate tumors



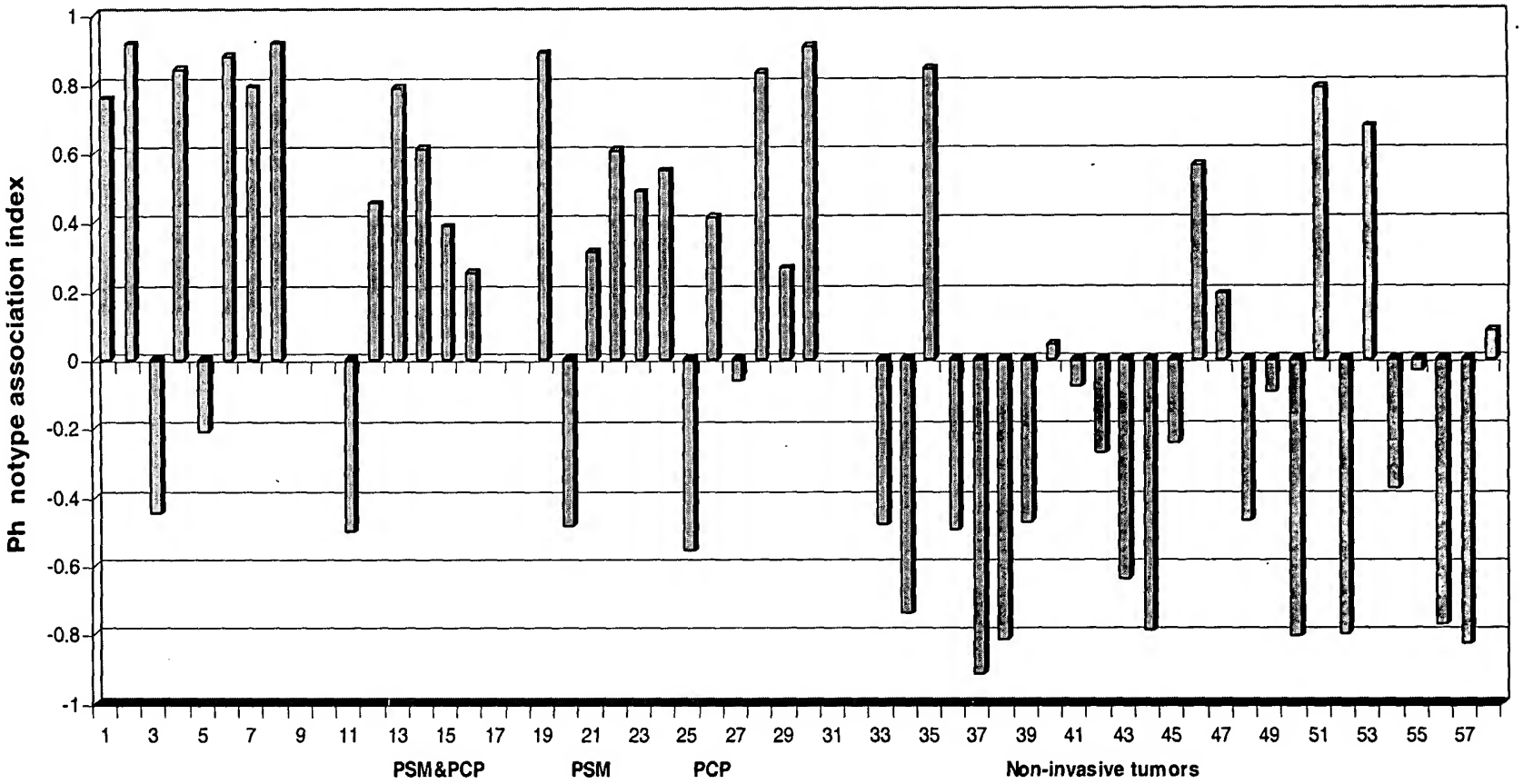
49C. Phenotype association indices of the 9 gene signature of the human prostate cancer metastasis in 9 metastatic and 23 primary human prostate tumors



49D. Phenotye association indices for transcripts of 6 prostate cancer metastasis signature gene clusters in 9 metastatic and 23 primary human prostate tumors



50A. Phenotype association indices for transcripts of the 5 genes prostate cancer invasion predictor cluster in 26 invasive and 26 non-invasive human prostate tumors



50B. Phenotype association indices for transcripts of the 8 genes prostate cancer recurrence predictor cluster in 8 recurrent and 13 non-recurrent human prostate tumors

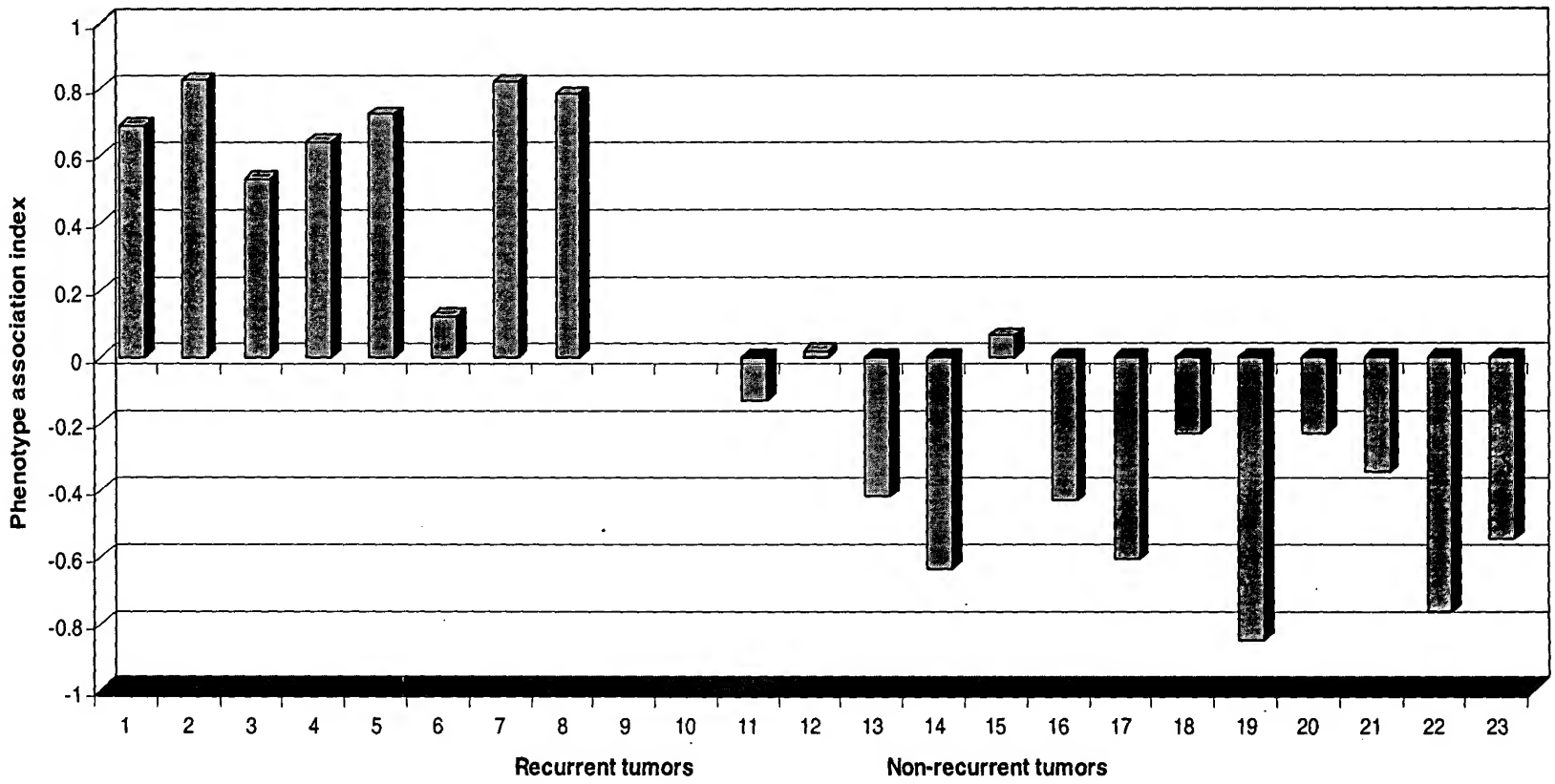


Figure 51A. Expression profiles of the 8 gene recurrence predictor signature in PC3MLN4 orthotopic xenografts and recurrent human prostate tumors

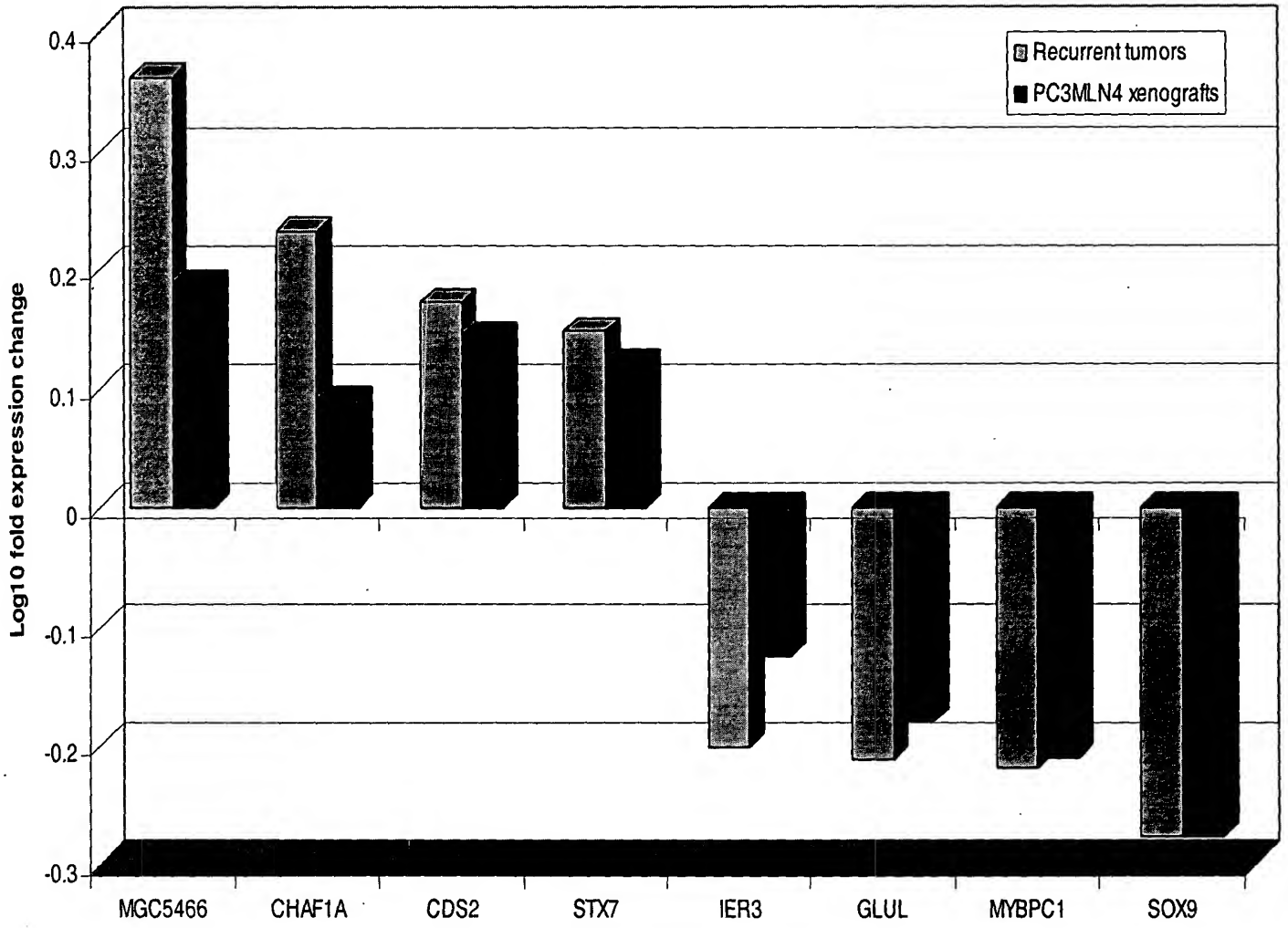


Figure 51B. Expression profiles of the 5 gene invasion signature in PC3MLN4 orthotopic xenografts and invasive human prostate tumors

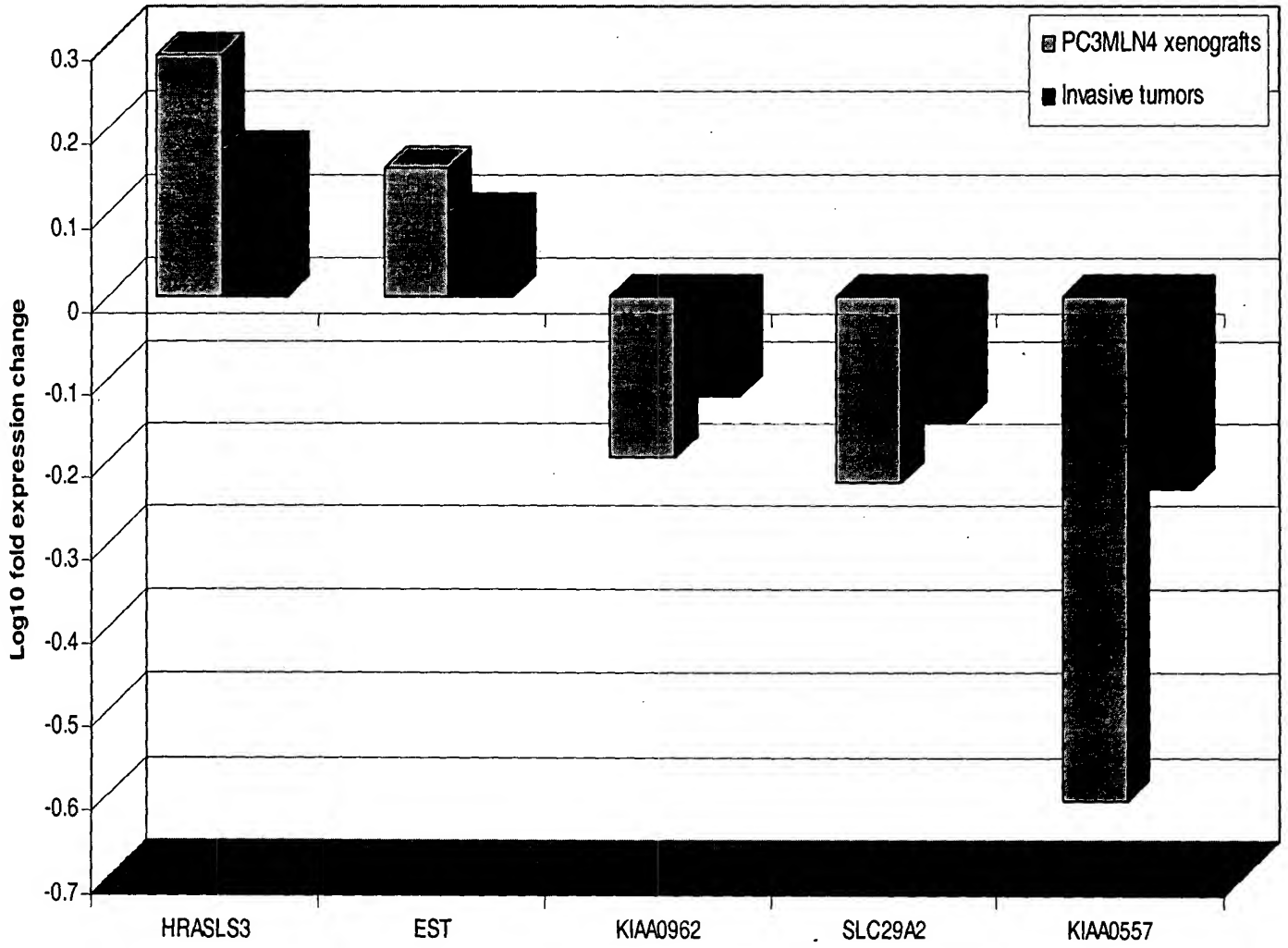


Figure 51C. Expression profiles of the 9 gene metastasis signature in PC3MLN4 orthotopic xenografts and metastatic human prostate tumors

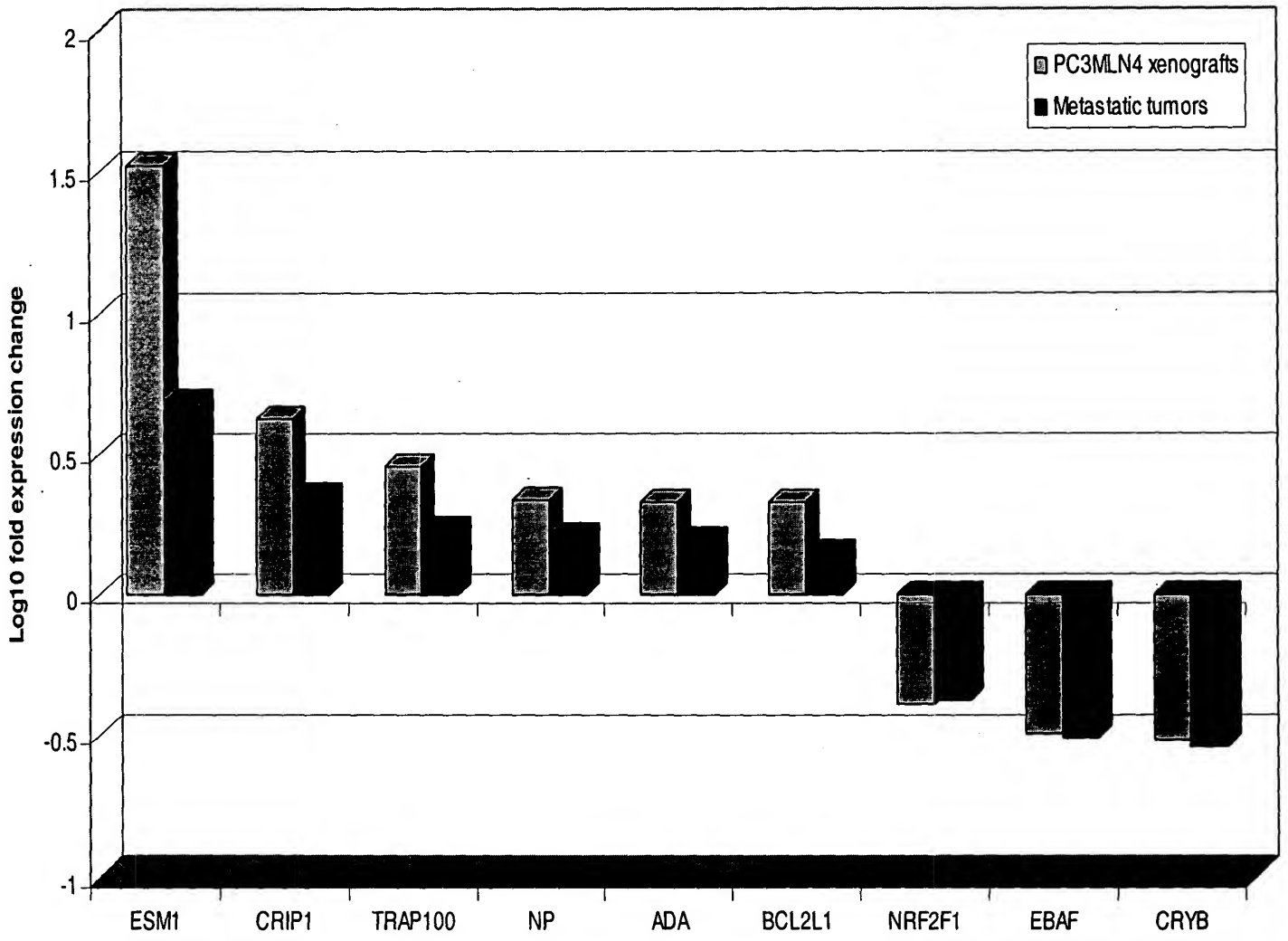


Figure 52A. Expression profiles of the 25 gene recurrence predictor signature in PC3MLN4 orthotopic xenografts and recurrent human prostate tumors

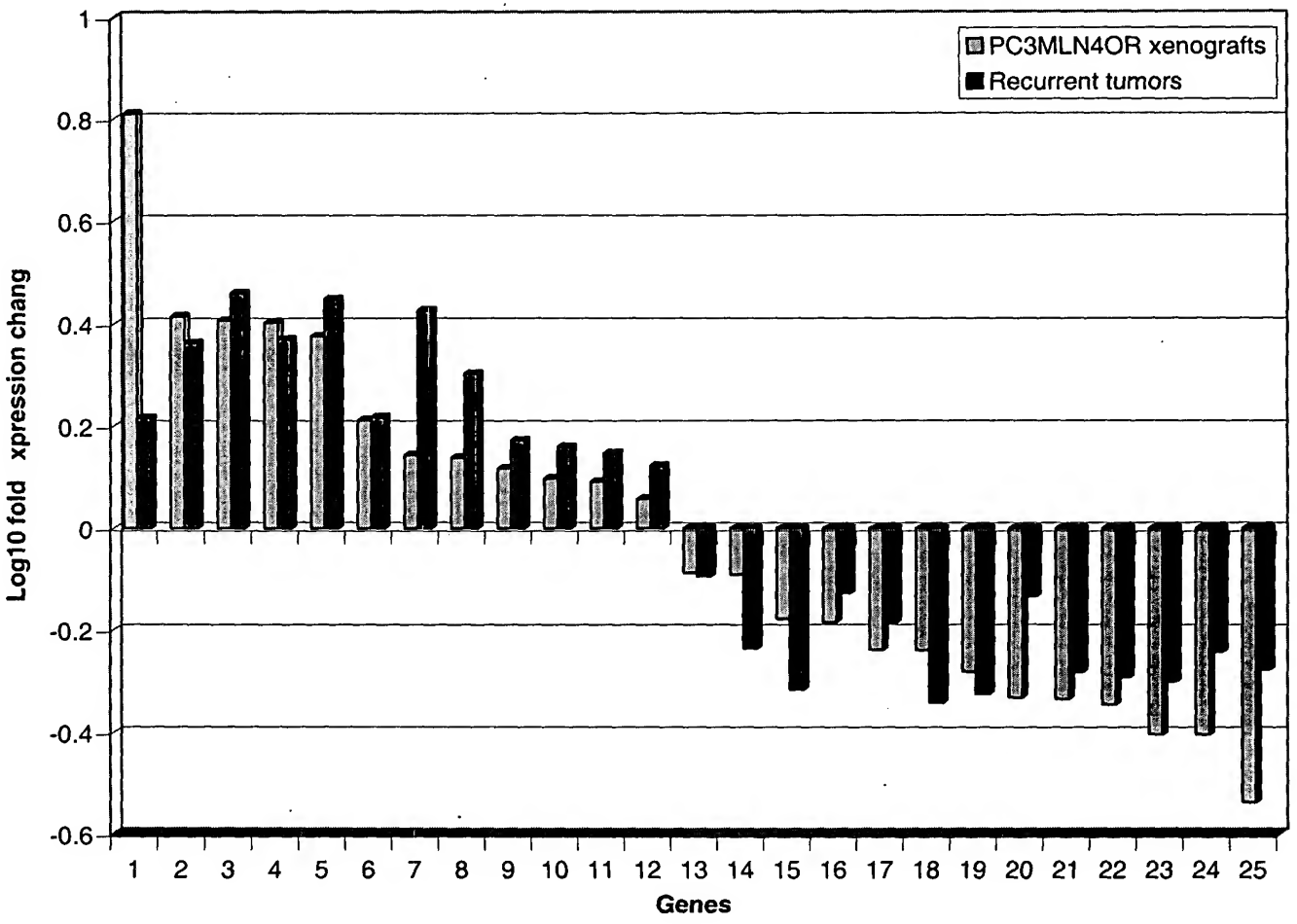


Figure 52B. Correlation of the expression profiles of the 25 genes recurrence predictor cluster in PC3MLN4 orthotopic xenografts and recurrent human prostate tumors

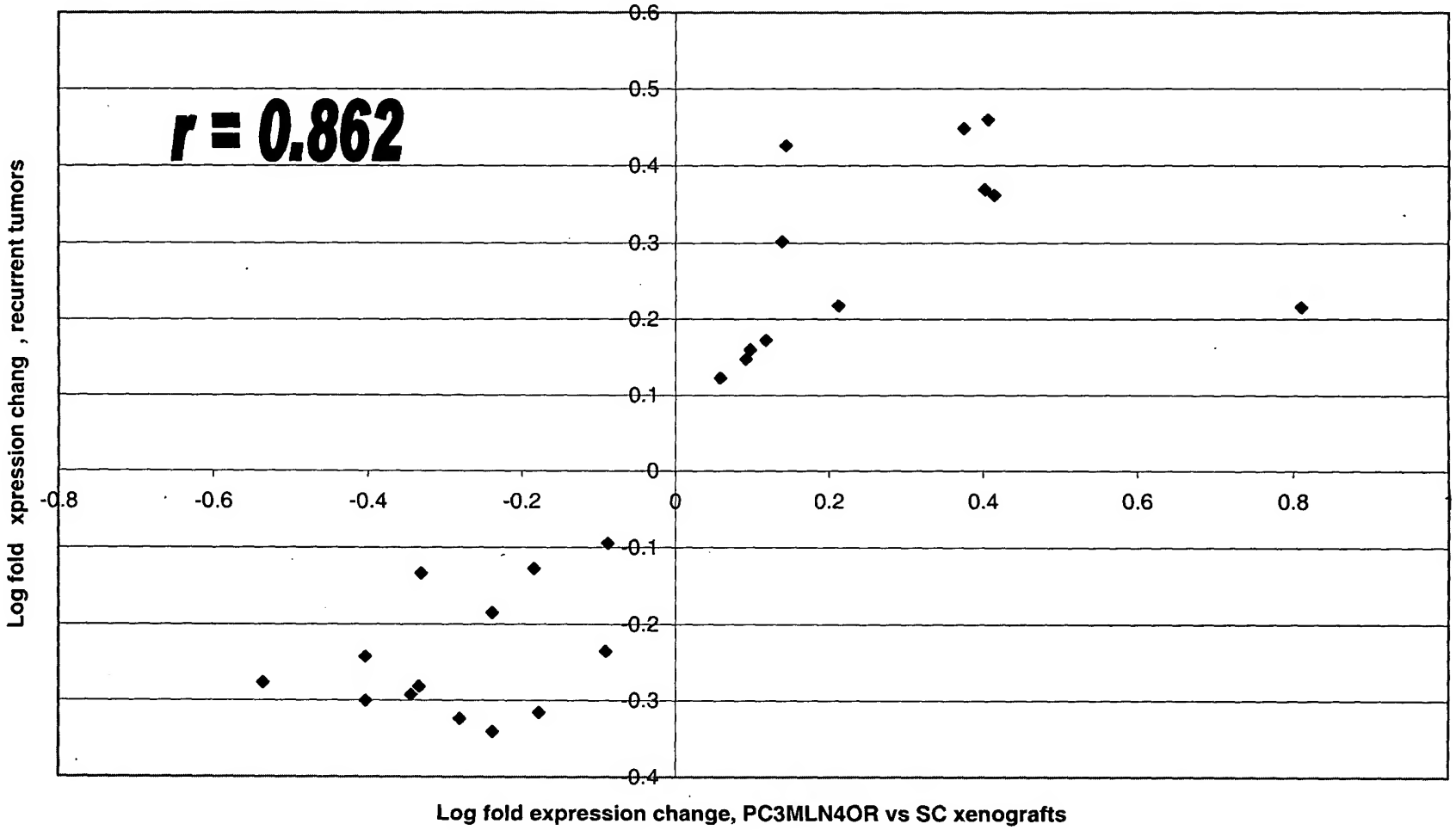


Figure 53. Phenotype association idices for transcripts of the 25 genes prostate cancer recurrence predictor cluster in 8 recurrent and 13 non-recurrent human prostate tumors

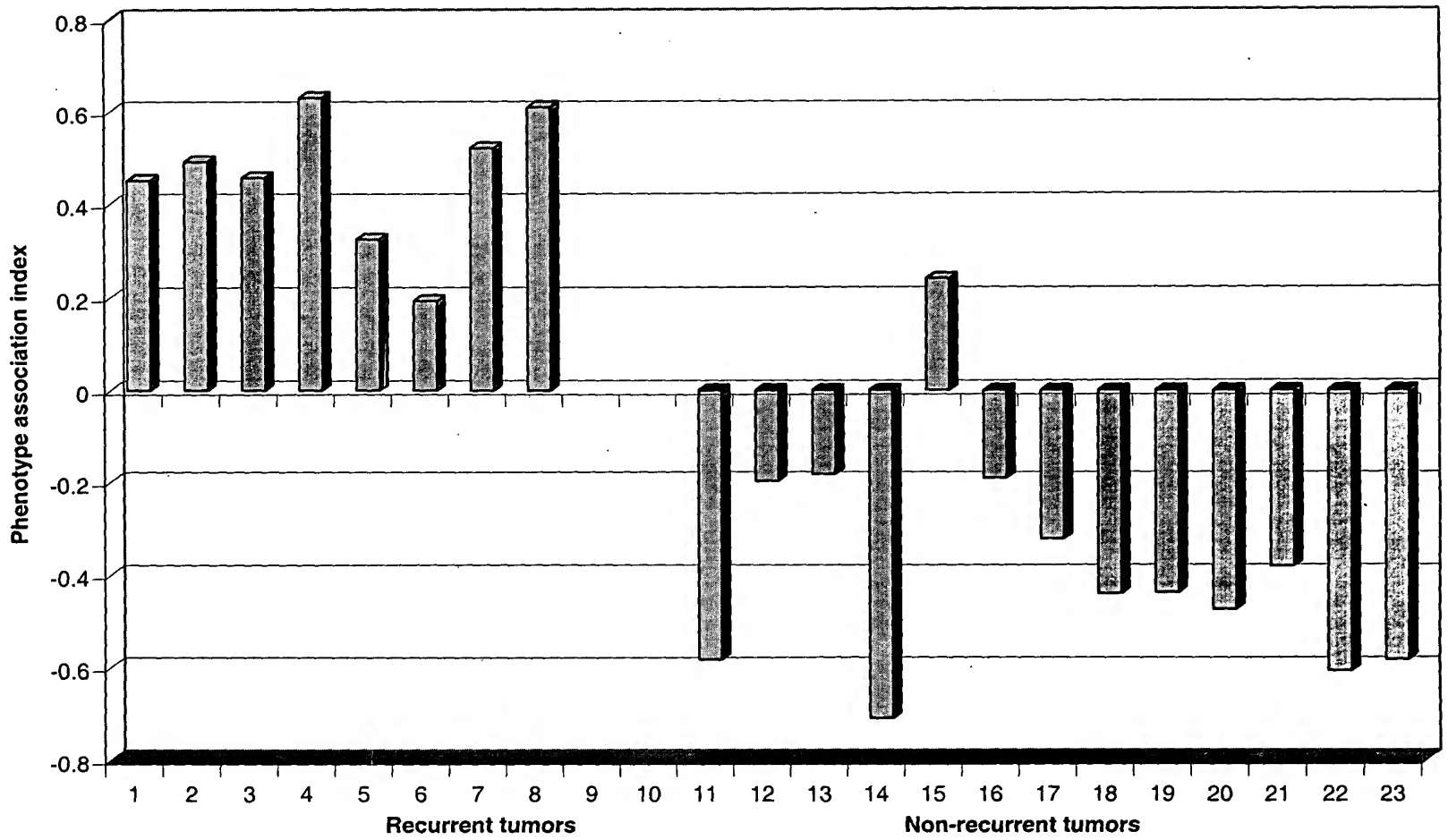


Figure 54. Expression profiles of the 12 gene recurrence predictor signature in PC3MLN4 orthotopic xenografts and recurrent human prostate tumors

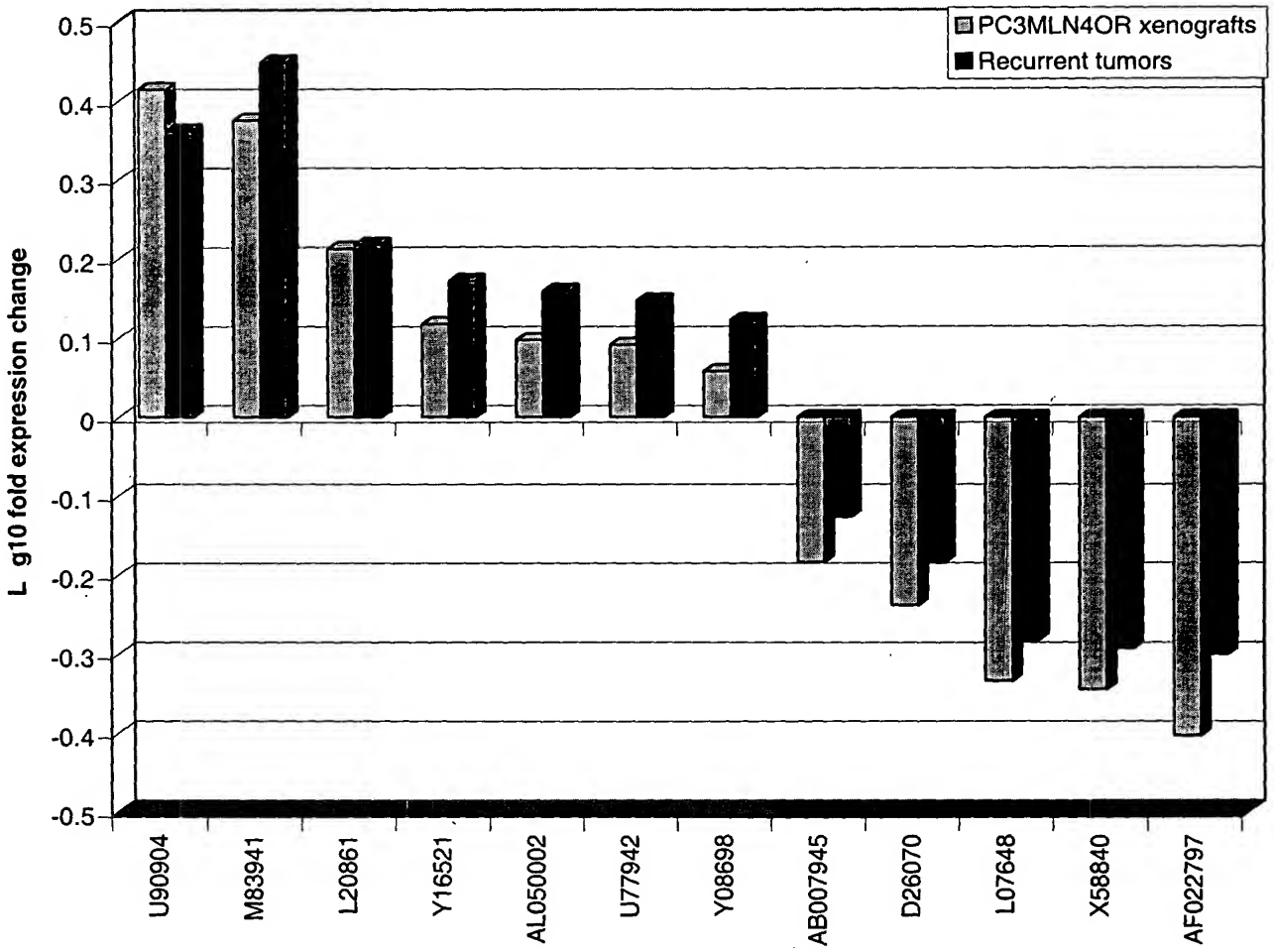


Figure 55. Correlation of the expression profiles of the 12 genes recurrence predictor cluster in PC3MLN4 orthotopic xenografts and recurrent human prostate tumors

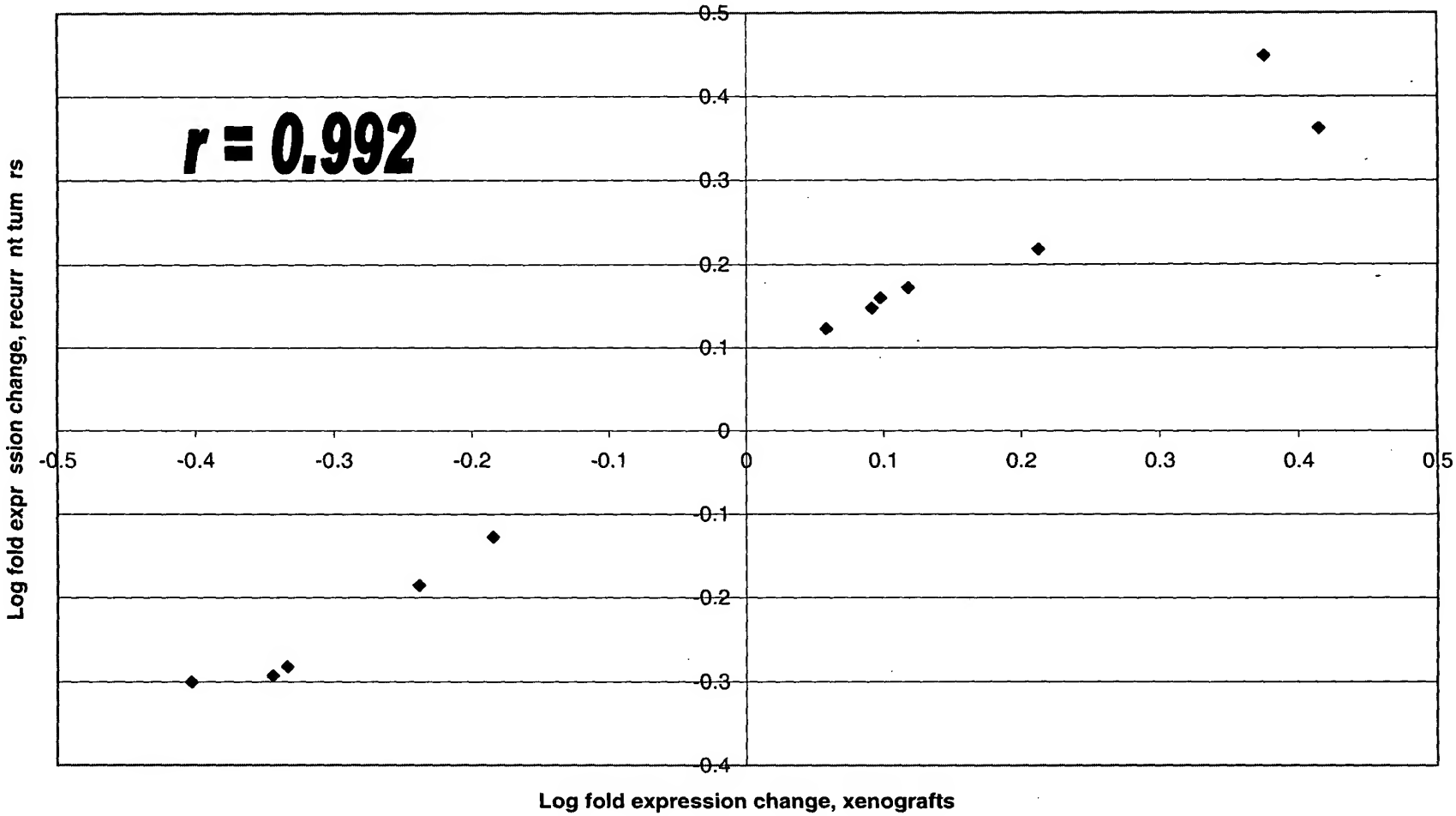


Figure 56. Phenotype association idices for transcripts of the 12 genes prostate cancer recurrence predictor cluster in 8 recurrent and 13 non-recurrent human prostate tumors

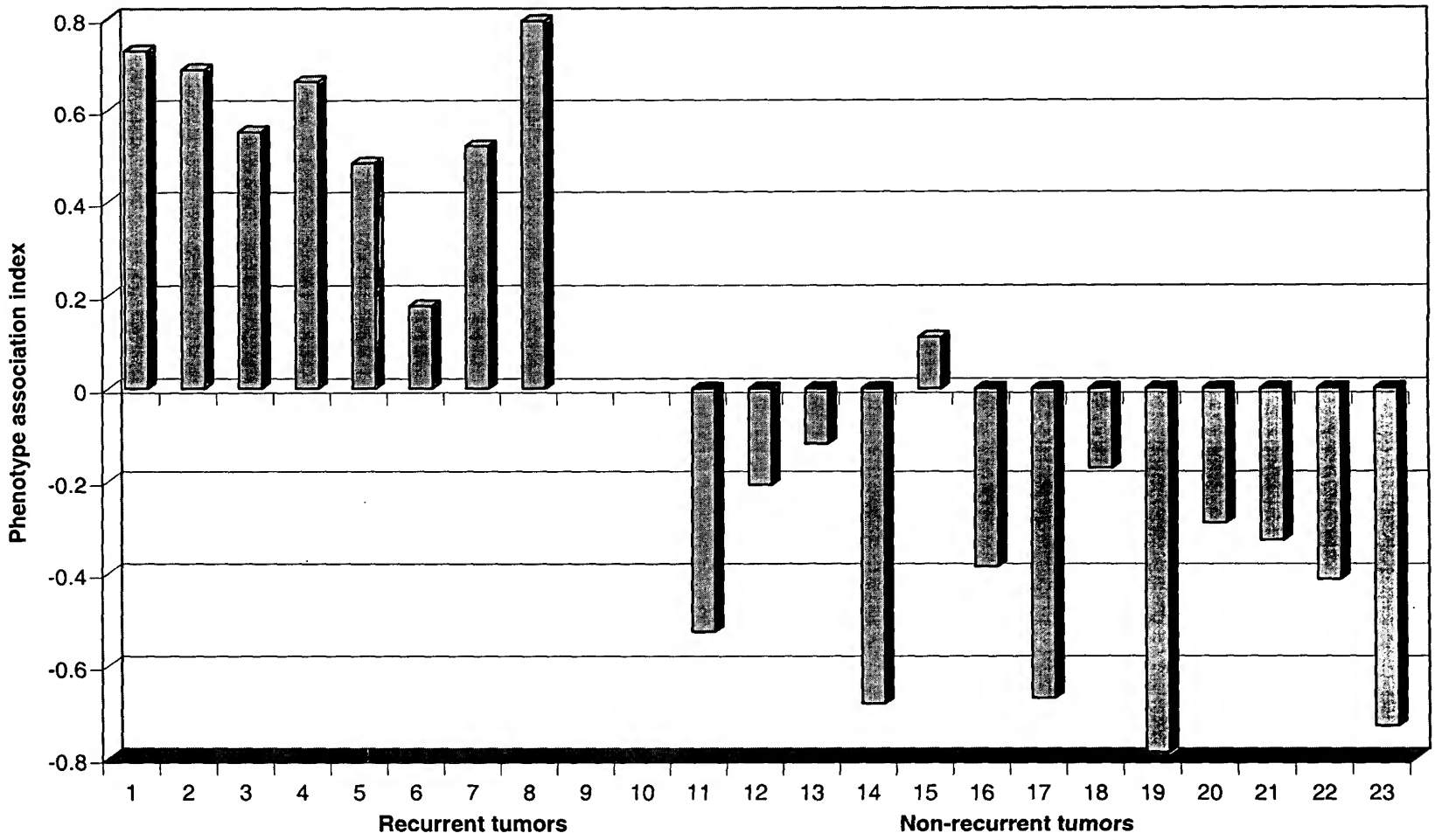
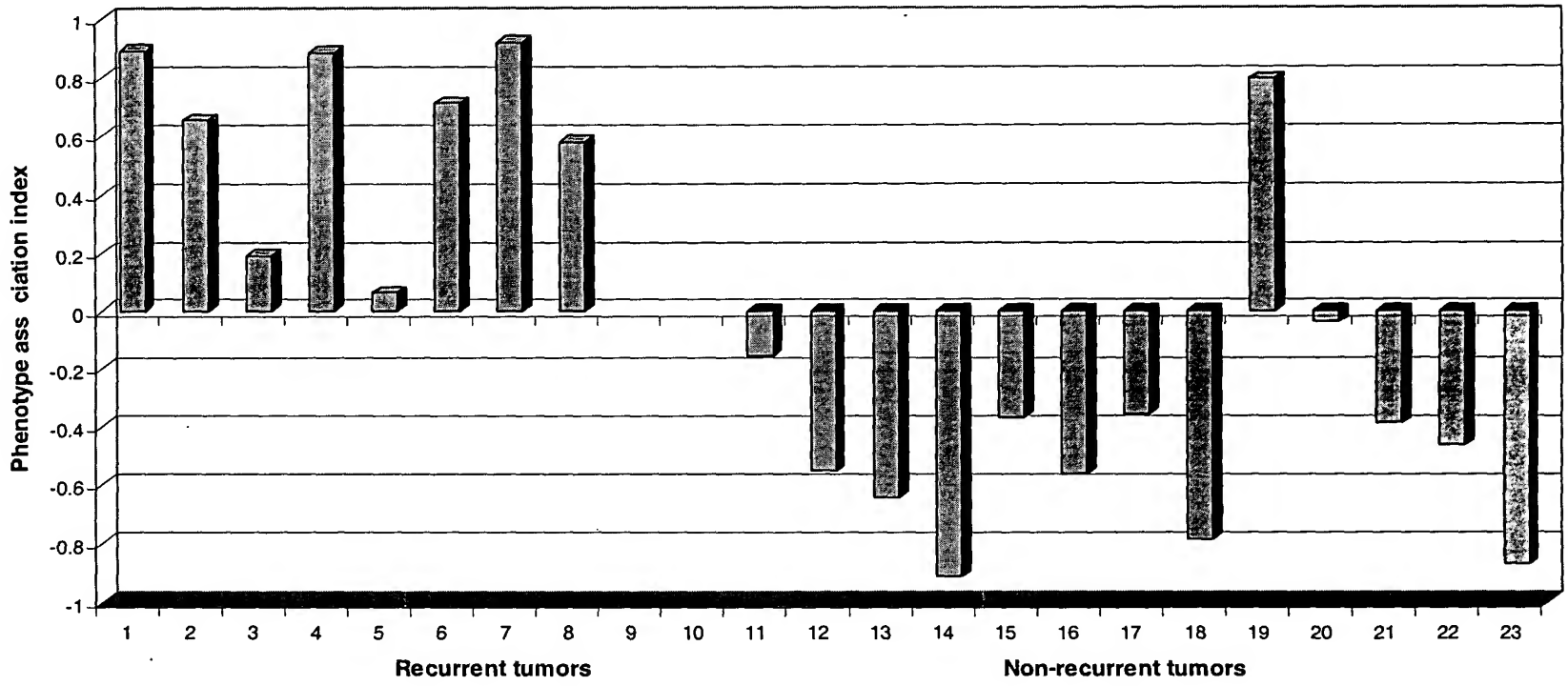
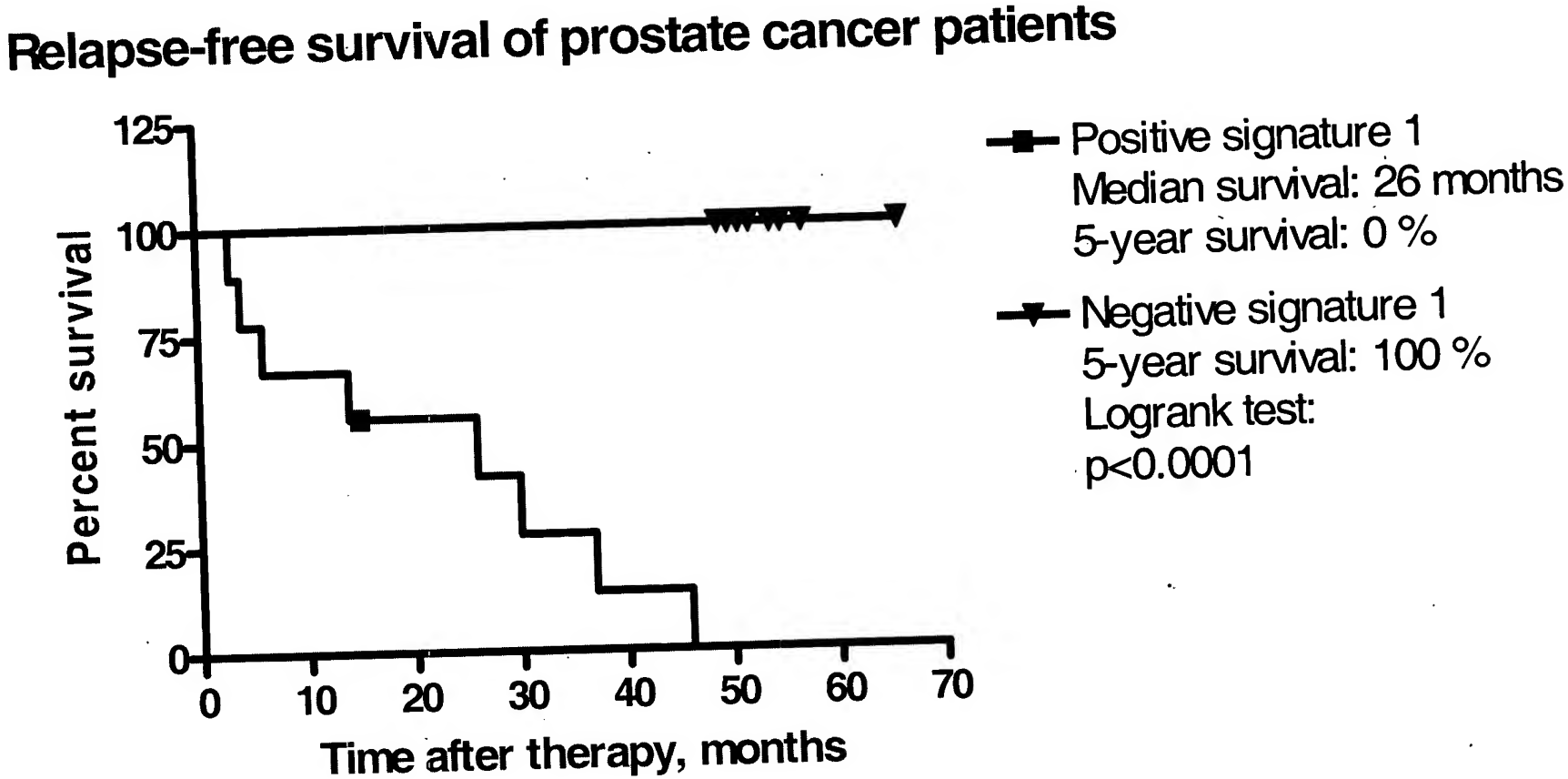


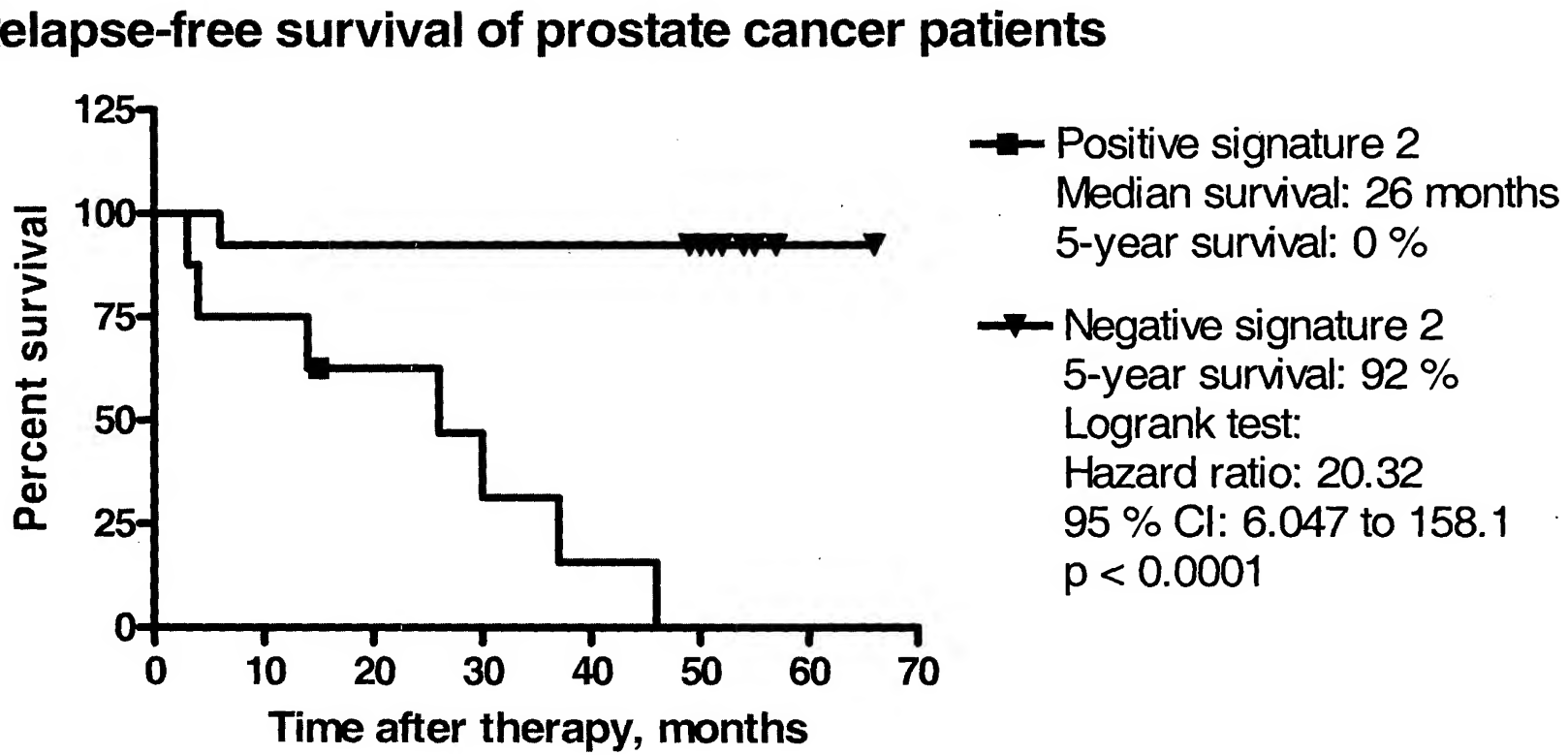
Figure 57. Phenotype association indices defined by expression profiles of transcripts of the recurrence predictor signature 1 in 8 recurrent and13 non-recurrent human prostate tumors



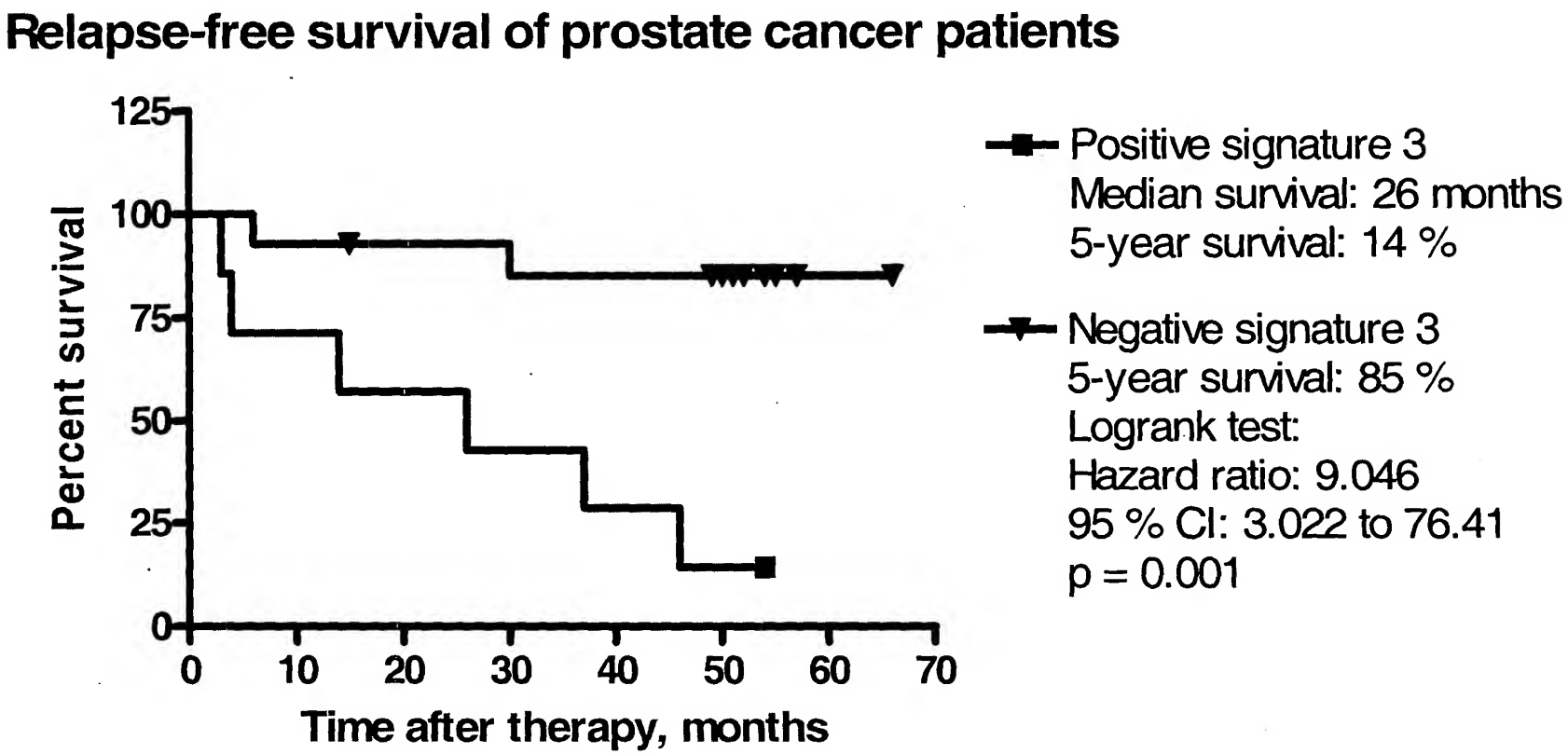
58A.


Relapse-free survival of prostate cancer patients
Percent survival
125
100
75
50
25
0
0
10
20
30
40
50
60
70
Time after therapy, months
Positive signature 1
Median survival: 26 months
5-year survival: 0 %
Negative signature 1
5-year survival: 100 %
Logrank test:
p<0.0001

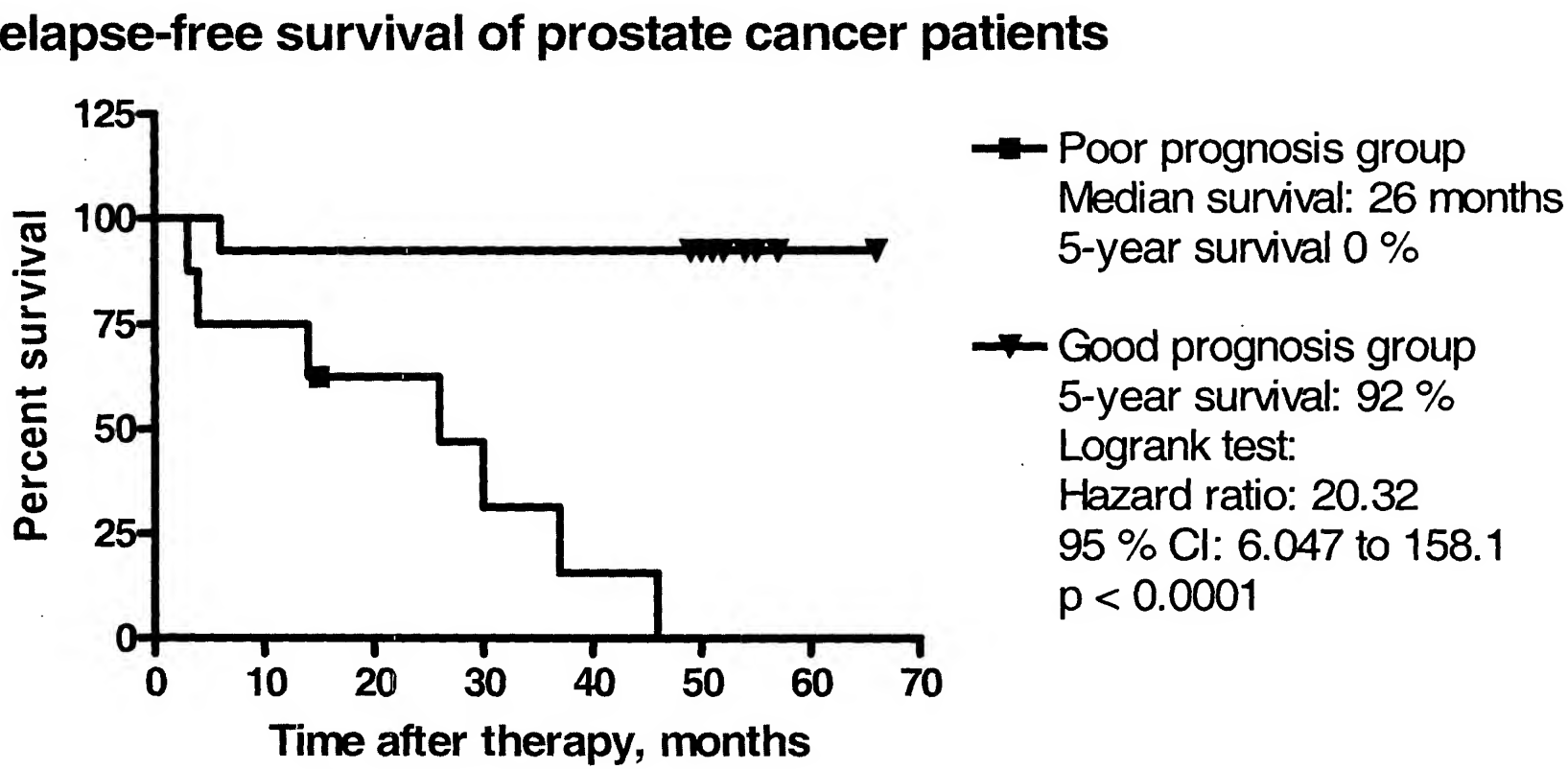
58B.


Relapse-free survival of prostate cancer patients
Percent survival
125
100
75
50
25
0
0
10
20
30
40
50
60
70
Time after therapy, months
Positive signature 2
Median survival: 26 months
5-year survival: 0 %
Negative signature 2
5-year survival: 92 %
Logrank test:
Hazard ratio: 20.32
95 % CI: 6.047 to 158.1
p < 0.0001

58C.

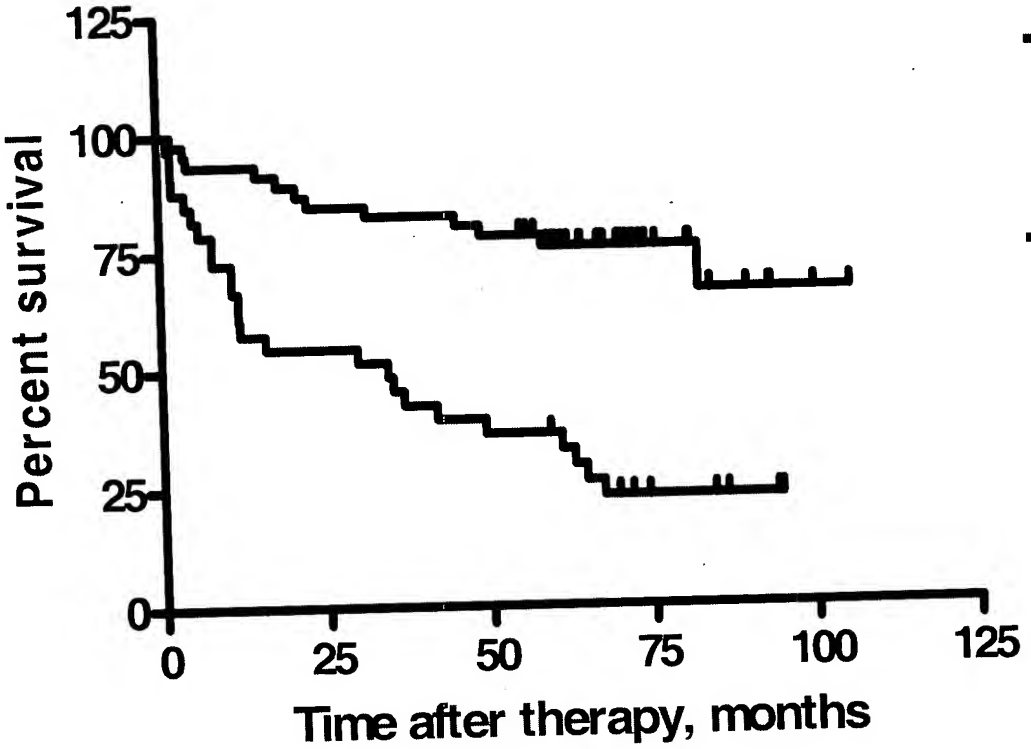

Relapse-free survival of prostate cancer patients
Percent survival
125
100
75
50
25
0
0
10
20
30
40
50
60
70
Time after therapy, months
Positive signature 3
Median survival: 26 months
5-year survival: 14 %
Negative signature 3
5-year survival: 85 %
Logrank test:
Hazard ratio: 9.046
95 % CI: 3.022 to 76.41
p = 0.001

58D.


Relapse-free survival of prostate cancer patients
Percent survival
125
100
75
50
25
0
0
10
20
30
40
50
60
70
Time after therapy, months
Poor prognosis group
Median survival: 26 months
5-year survival 0 %
Good prognosis group
5-year survival: 92 %
Logrank test:
Hazard ratio: 20.32
95 % CI: 6.047 to 158.1
p < 0.0001

59A.

Relapse-free survival of prostate cancer patients

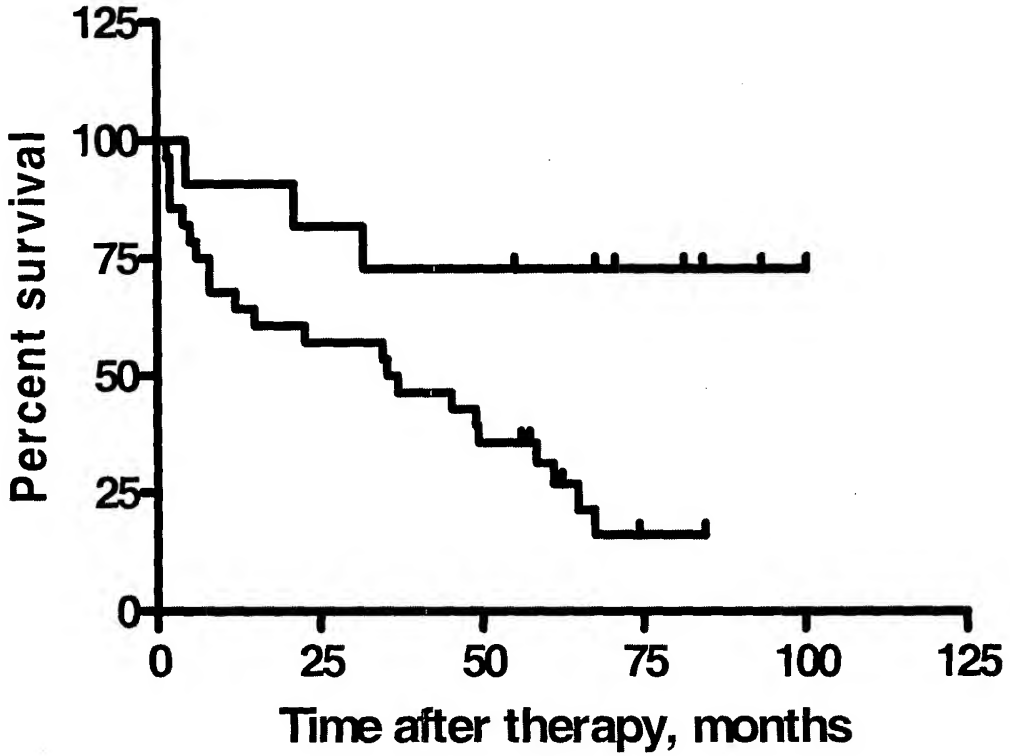


Poor prognosis group
Median survival: 34.6 months
5-year survival: 33 %

Good prognosis group
5-year survival: 76 %
Logrank test:
Hazard ratio: 4.224
95 % CI: 2.455 to 9.781
$p < 0.0001$

59B

Relapse-free survival of prostate cancer patients with high preoperative PSA level

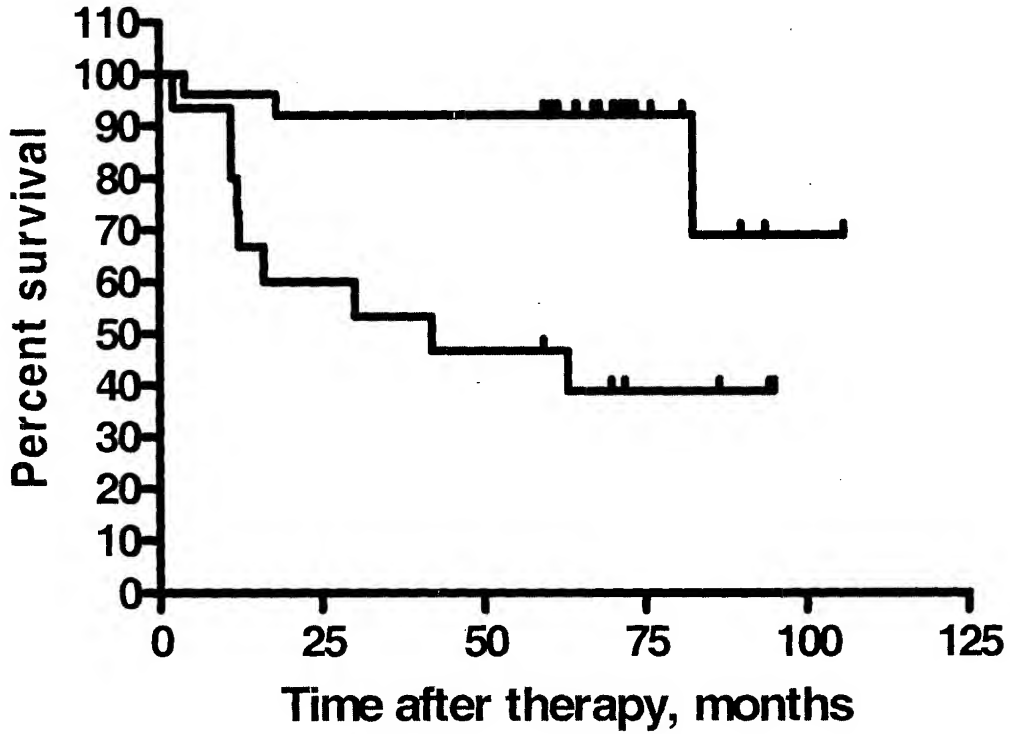


Poor prognosis group
Median survival: 36.2 months
5-year survival: 27 %

Good prognosis goup
5-year survival: 73%
Logrank test:
Hazard ratio: 4.315
95 % CI: 1.338 to 7.025
p = 0.0081

59C.

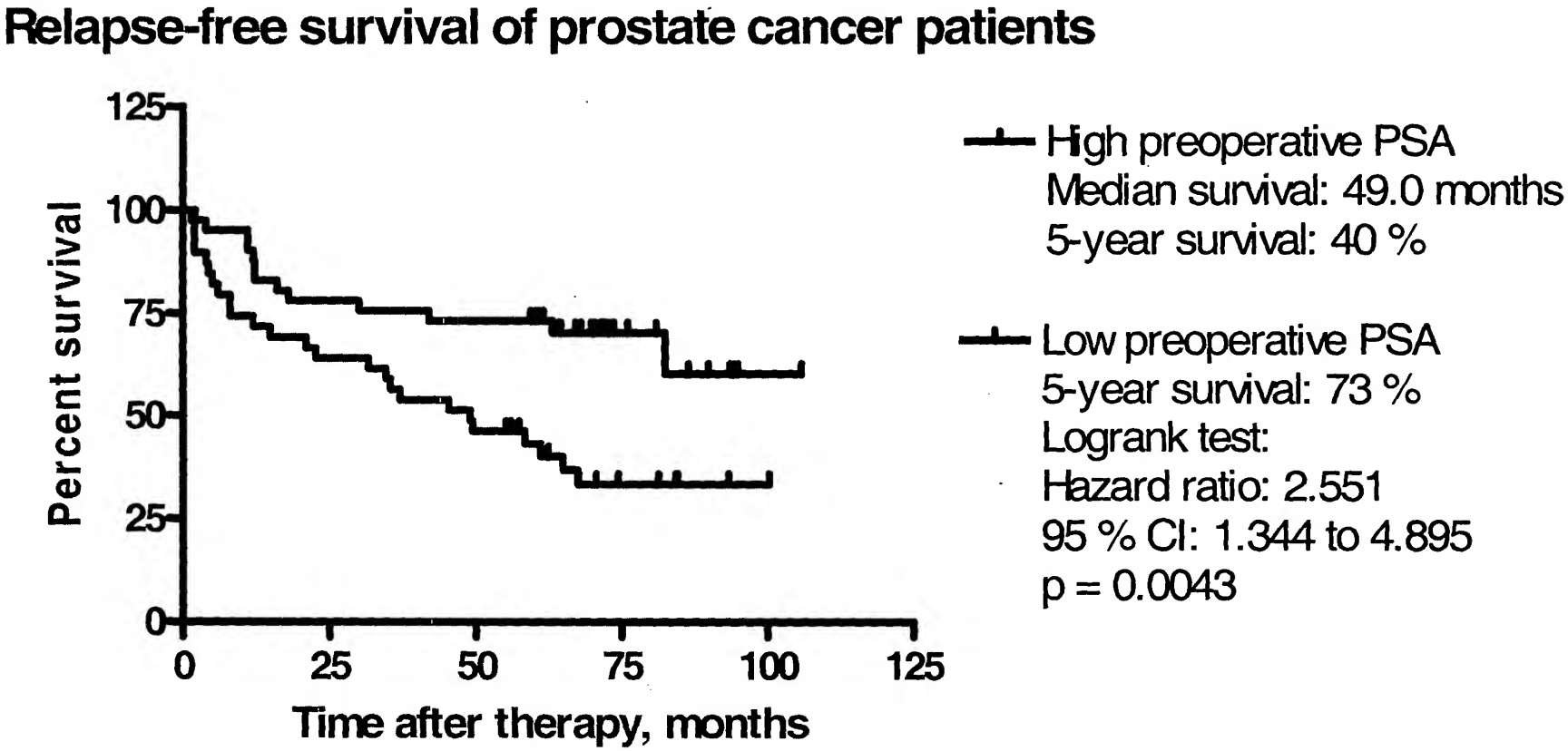
Relapse-free survival of prostate cancer patients with low preoperative PSA level



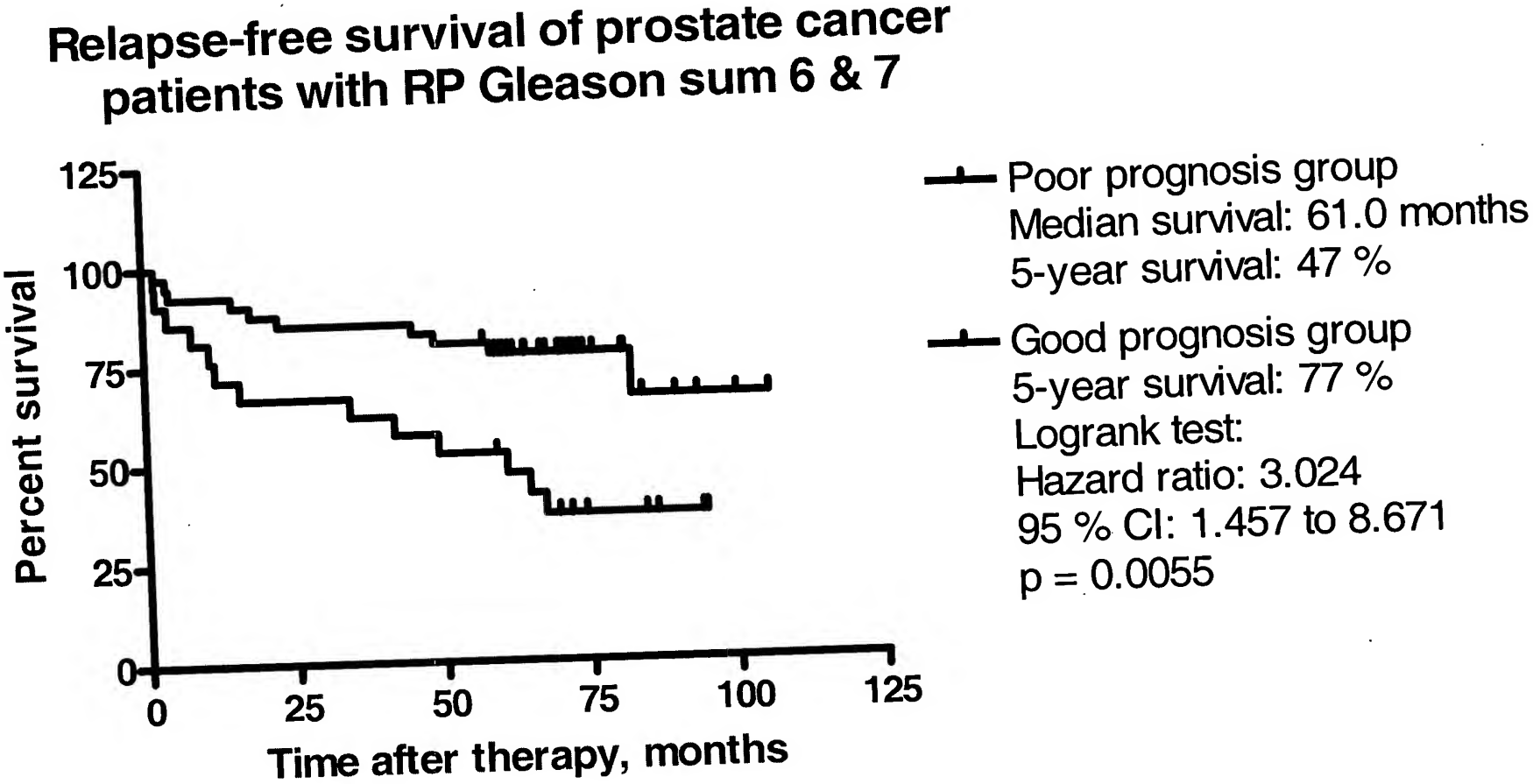
Poor prognosis group
Median survival: 42.0 months
5-year survival: 47 %

Good prognosis group
5-year survival: 92 %
Logrank test:
Hazard ratio: 6.247
95 % CI: 2.134 to 24.48
p = 0.0015

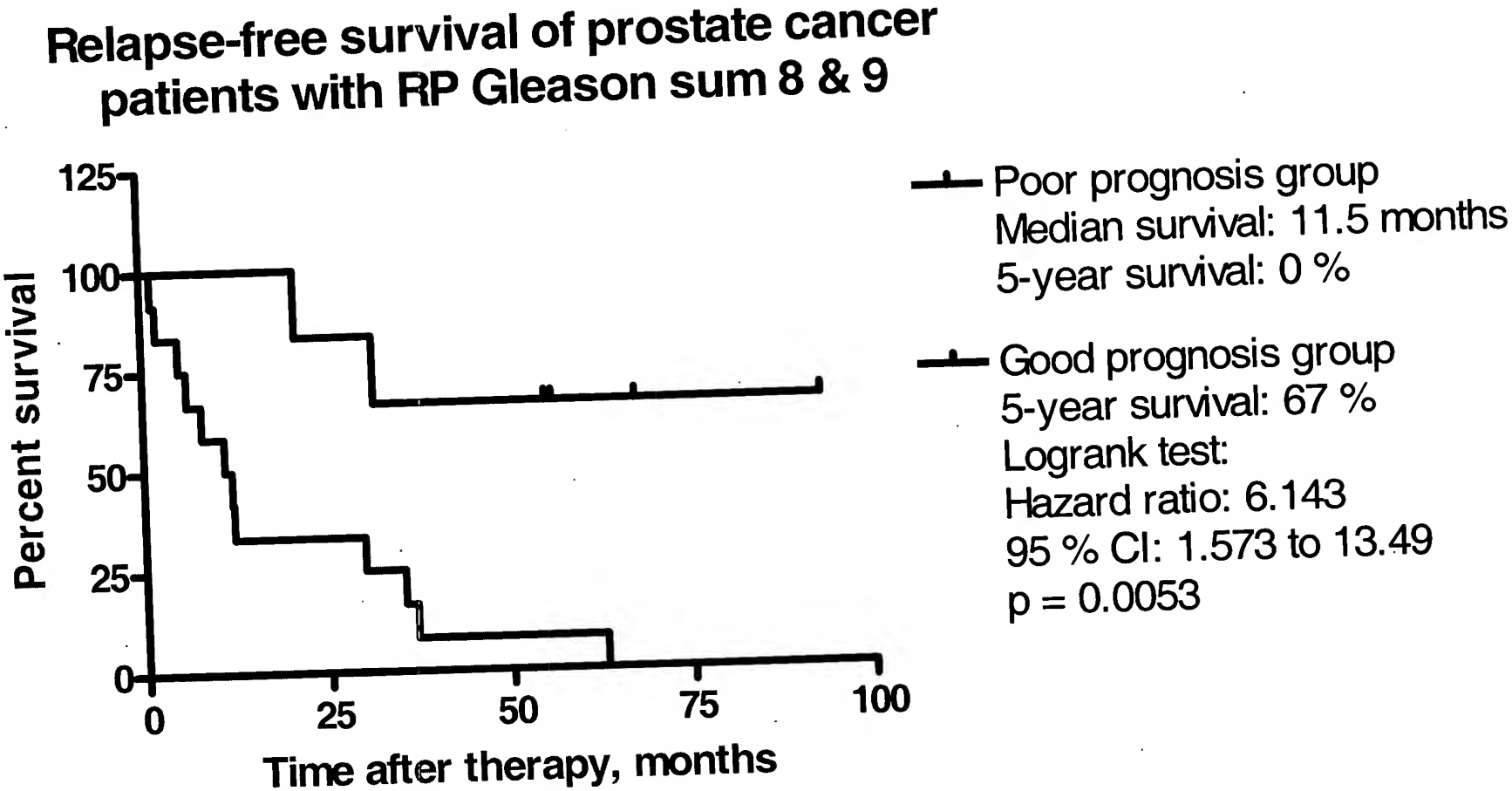
59D.


Relapse-free survival of prostate cancer patients
Percent survival
125
100
75
50
25
0
0
25
50
75
100
125
Time after therapy, months
High preoperative PSA
Median survival: 49.0 months
5-year survival: 40 %
Low preoperative PSA
5-year survival: 73 %
Logrank test:
Hazard ratio: 2.551
95 % CI: 1.344 to 4.895
p = 0.0043

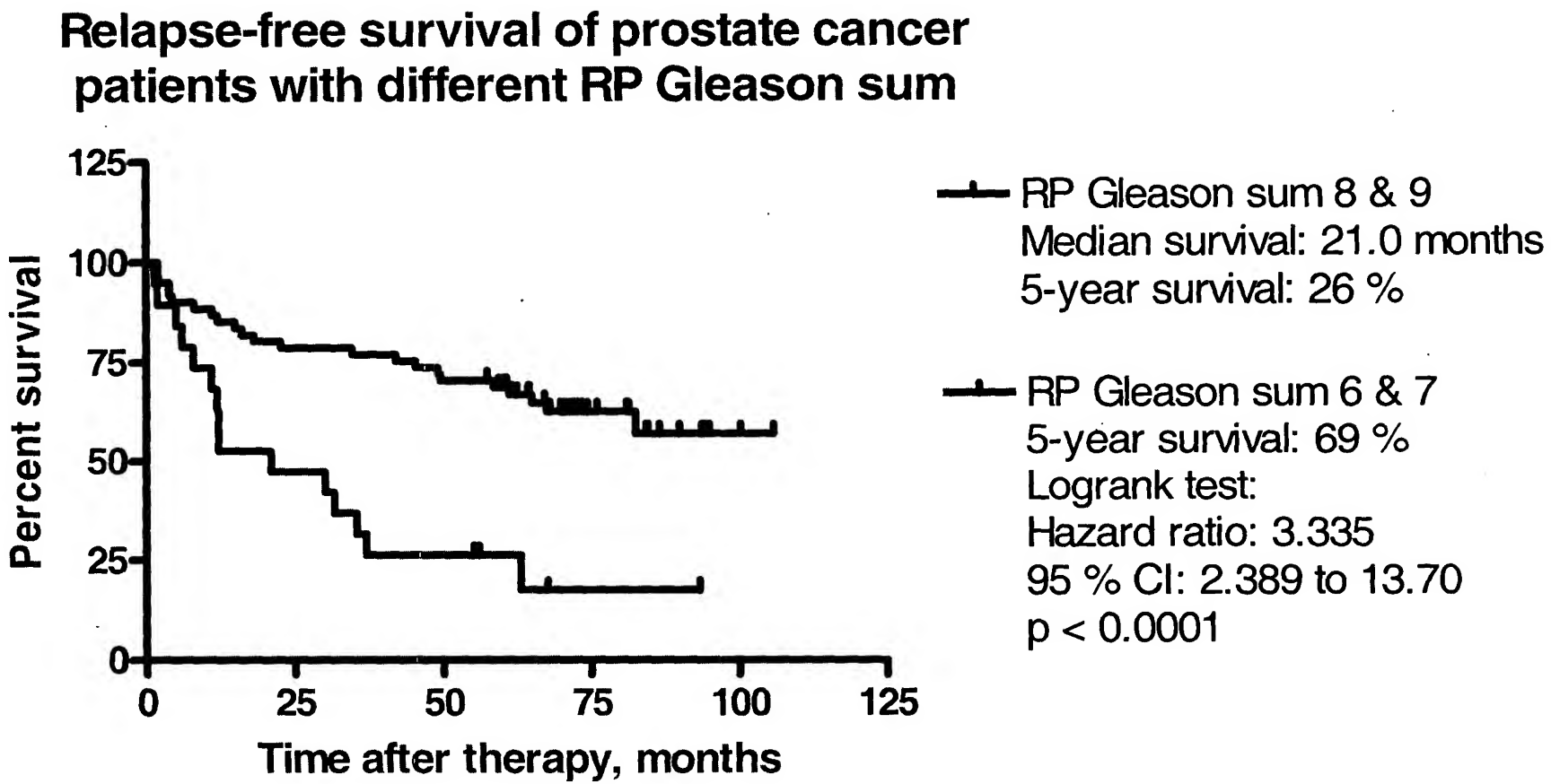
60A.


Relapse-free survival of prostate cancer patients with RP Gleason sum 6 & 7
Percent survival
125
100
75
50
25
0
0
25
50
75
100
125
Time after therapy, months
Poor prognosis group
Median survival: 61.0 months
5-year survival: 47 %
Good prognosis group
5-year survival: 77 %
Logrank test:
Hazard ratio: 3.024
95 % CI: 1.457 to 8.671
p = 0.0055

60B

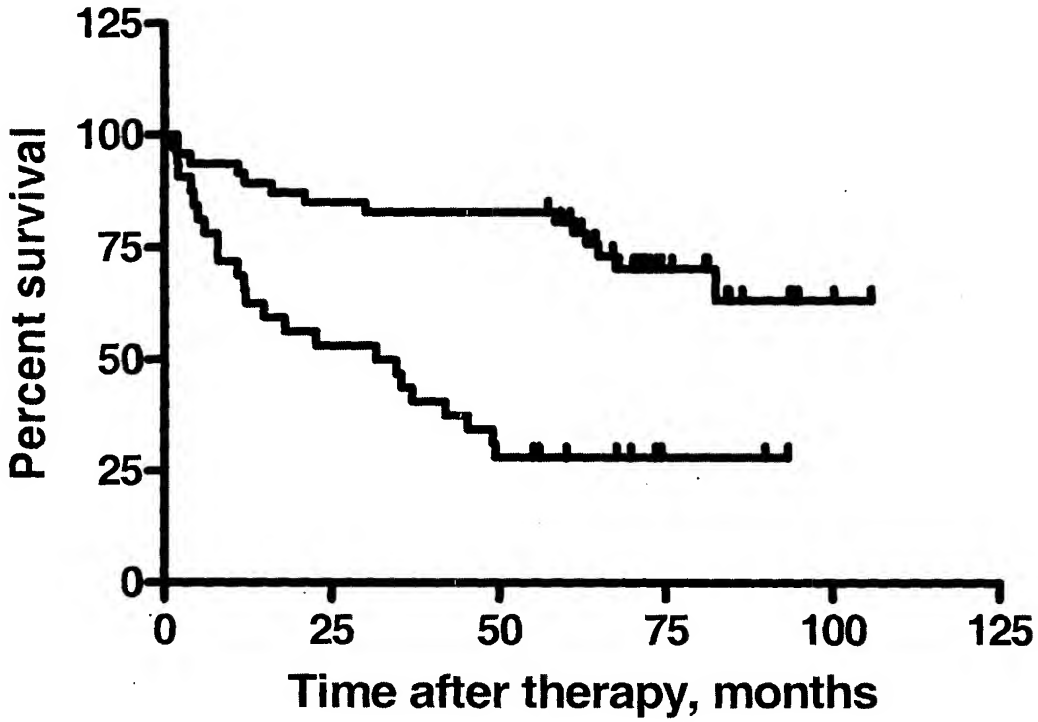

Relapse-free survival of prostate cancer patients with RP Gleason sum 8 & 9
Percent survival
125
100
75
50
25
0
0
25
50
75
100
Time after therapy, months
Poor prognosis group
Median survival: 11.5 months
5-year survival: 0 %
Good prognosis group
5-year survival: 67 %
Logrank test:
Hazard ratio: 6.143
95 % CI: 1.573 to 13.49
p = 0.0053

60C


Relapse-free survival of prostate cancer patients with different RP Gleason sum
Percent survival
125
100
75
50
25
0
0
25
50
75
100
125
Time after therapy, months
RP Gleason sum 8 & 9
Median survival: 21.0 months
5-year survival: 26 %
RP Gleason sum 6 & 7
5-year survival: 69 %
Logrank test:
Hazard ratio: 3.335
95 % CI: 2.389 to 13.70
p < 0.0001

61A

Relapse-free survival of prostate cancer patients in distinct nomogram-defined subgroups



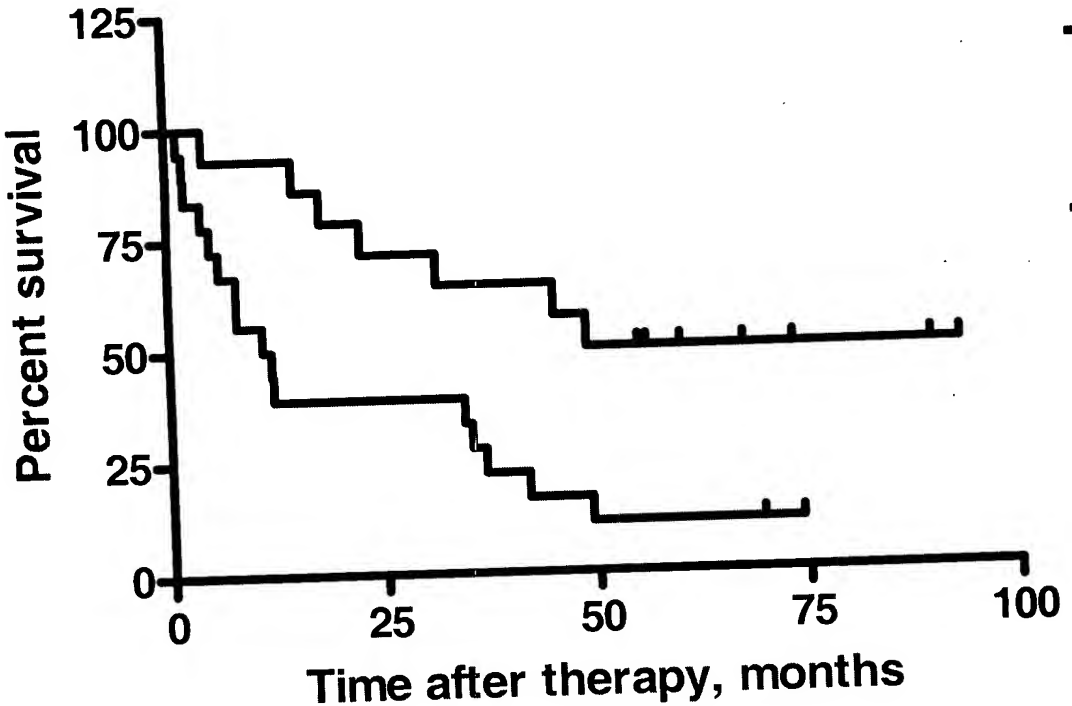
Poor prognosis group
Median survival: 33.1 months
5-year survival: 28 %

Good prognosis group
5-year survival: 81 %

Logrank test:
Hazard ratio: 3.757
95 % CI: 2.318 to 9.647
$p < 0.0001$

61B

Relapse-free survival of prostate cancer patients (nomogram-defined poor prognosis group)

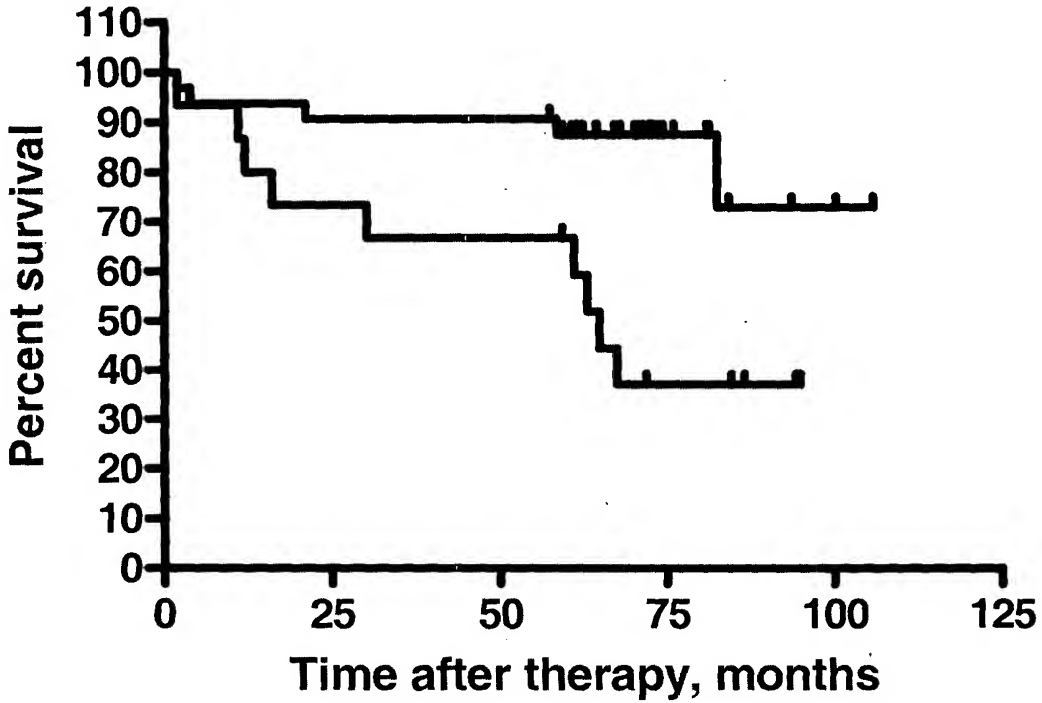


Poor prognosis signature
Meidan survival: 11.5 months
5-year survival: 11 %

Good prognosis signature
Median survival: 71.1 months
5-year survival: 50 %
Logrank test:
Hazard ratio: 3.129
95 % CI: 1.378 to 7.434
p = 0.0068

61C.

Relapse-free survival of prostate cancer patients (nomogram-defined good prognosis group)

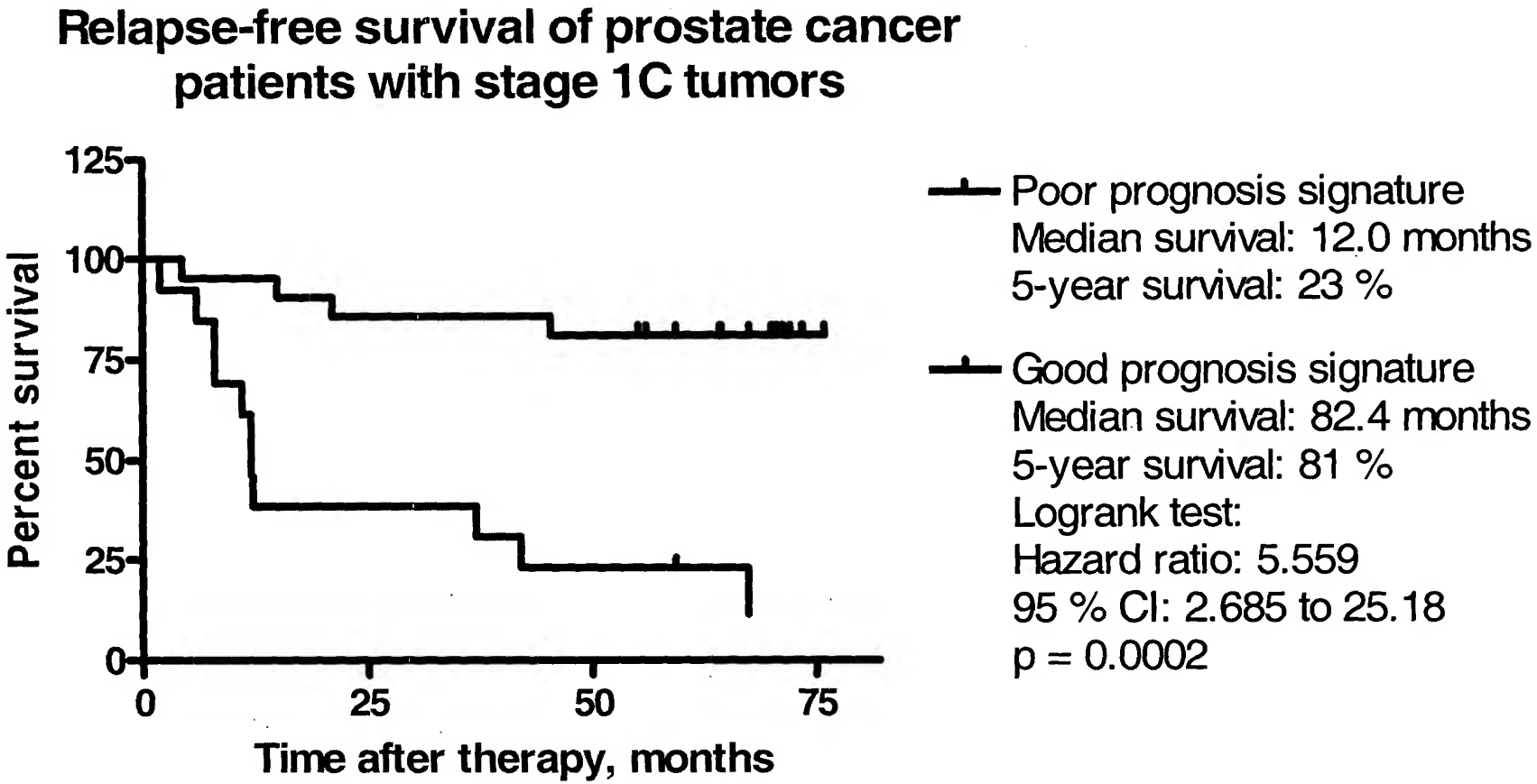


Poor prognosis signature
Median survival: 64.8 months
5-year survival: 59 %

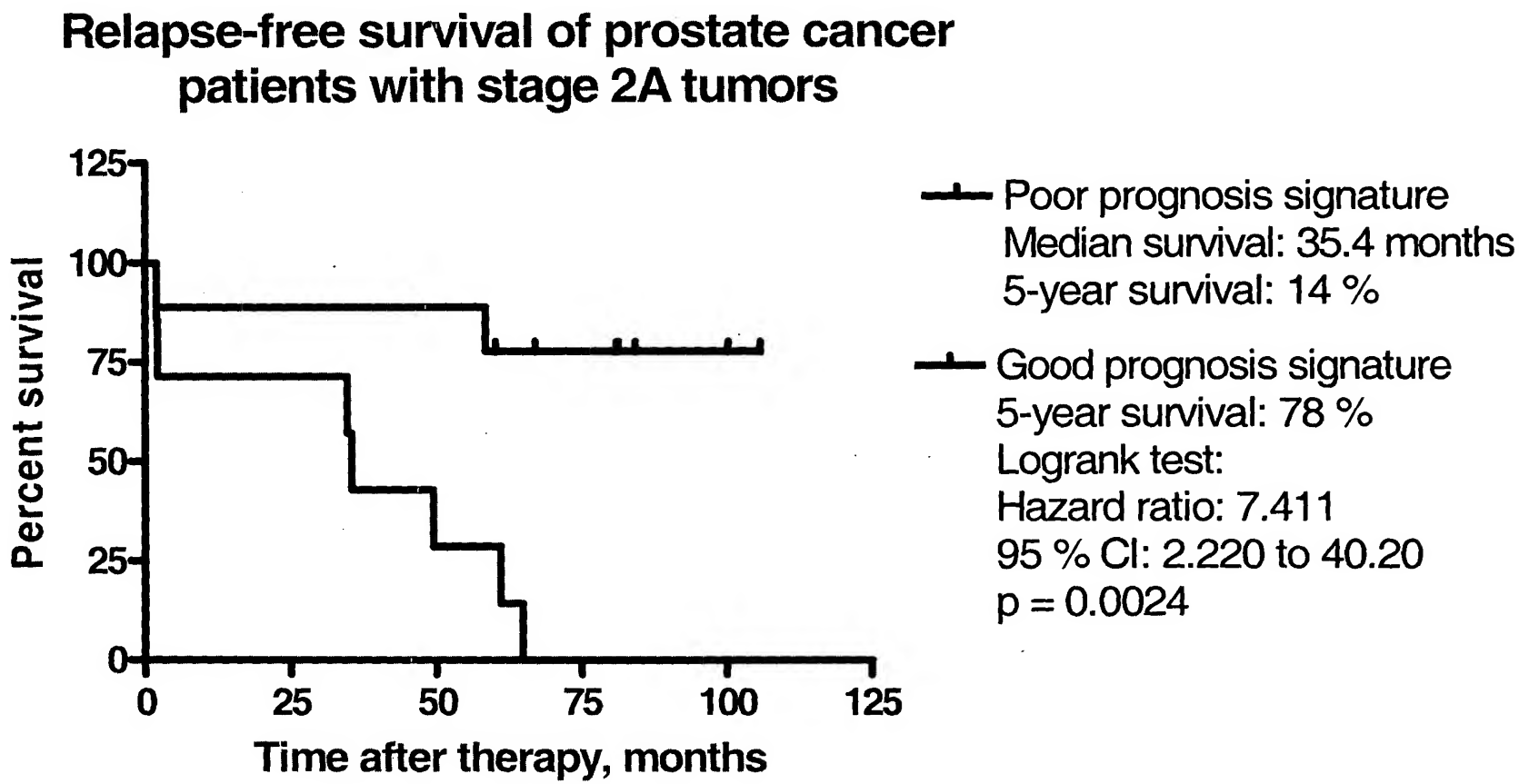
Good prognosis signature
5-year survival: 87 %

Logrank test:
Hazard ratio: 4.398
95 % CI: 1.767 to 18.00
p = 0.0035

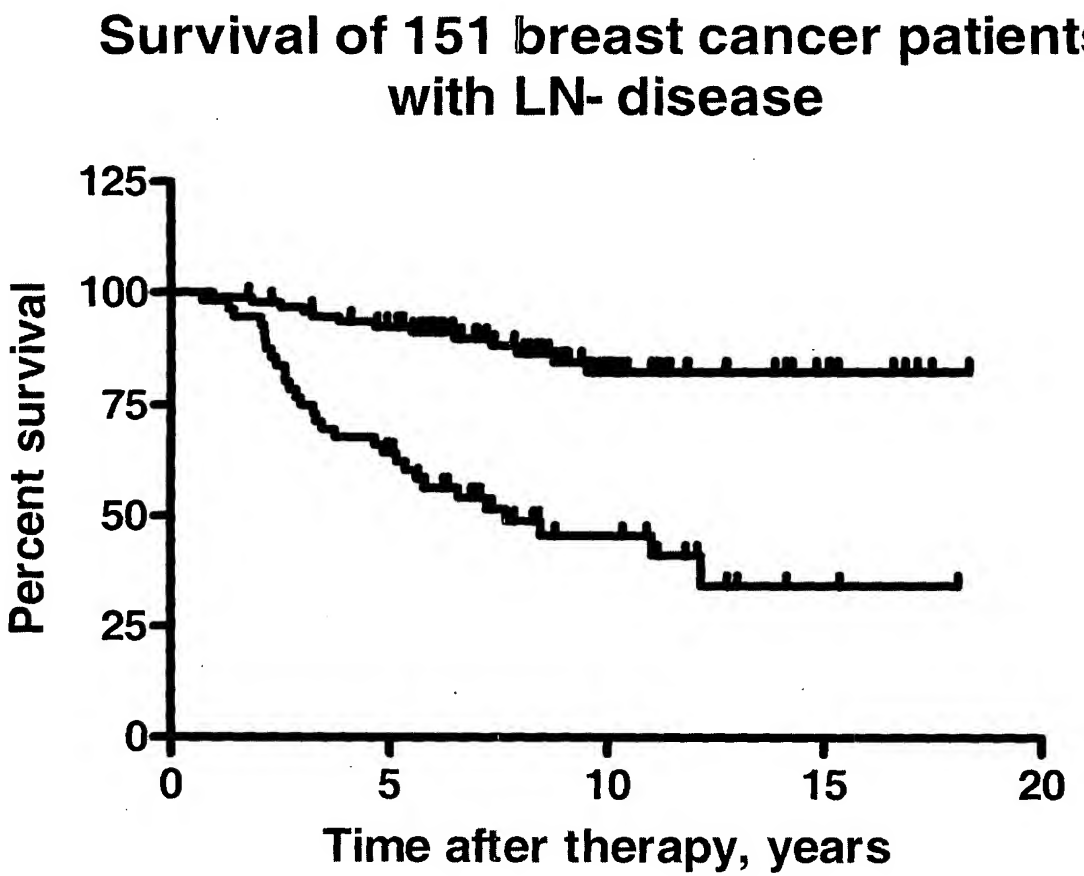
62A.


Relapse-free survival of prostate cancer patients with stage 1C tumors
Percent survival
125
100
75
50
25
0
0
25
50
75
Time after therapy, months
Poor prognosis signature
Median survival: 12.0 months
5-year survival: 23 %
Good prognosis signature
Median survival: 82.4 months
5-year survival: 81 %
Logrank test:
Hazard ratio: 5.559
95 % CI: 2.685 to 25.18
p = 0.0002

62B.


Relapse-free survival of prostate cancer patients with stage 2A tumors
Percent survival
125
100
75
50
25
0
0
25
50
75
100
125
Time after therapy, months
Poor prognosis signature
Median survival: 35.4 months
5-year survival: 14 %
Good prognosis signature
5-year survival: 78 %
Logrank test:
Hazard ratio: 7.411
95 % CI: 2.220 to 40.20
p = 0.0024

63A

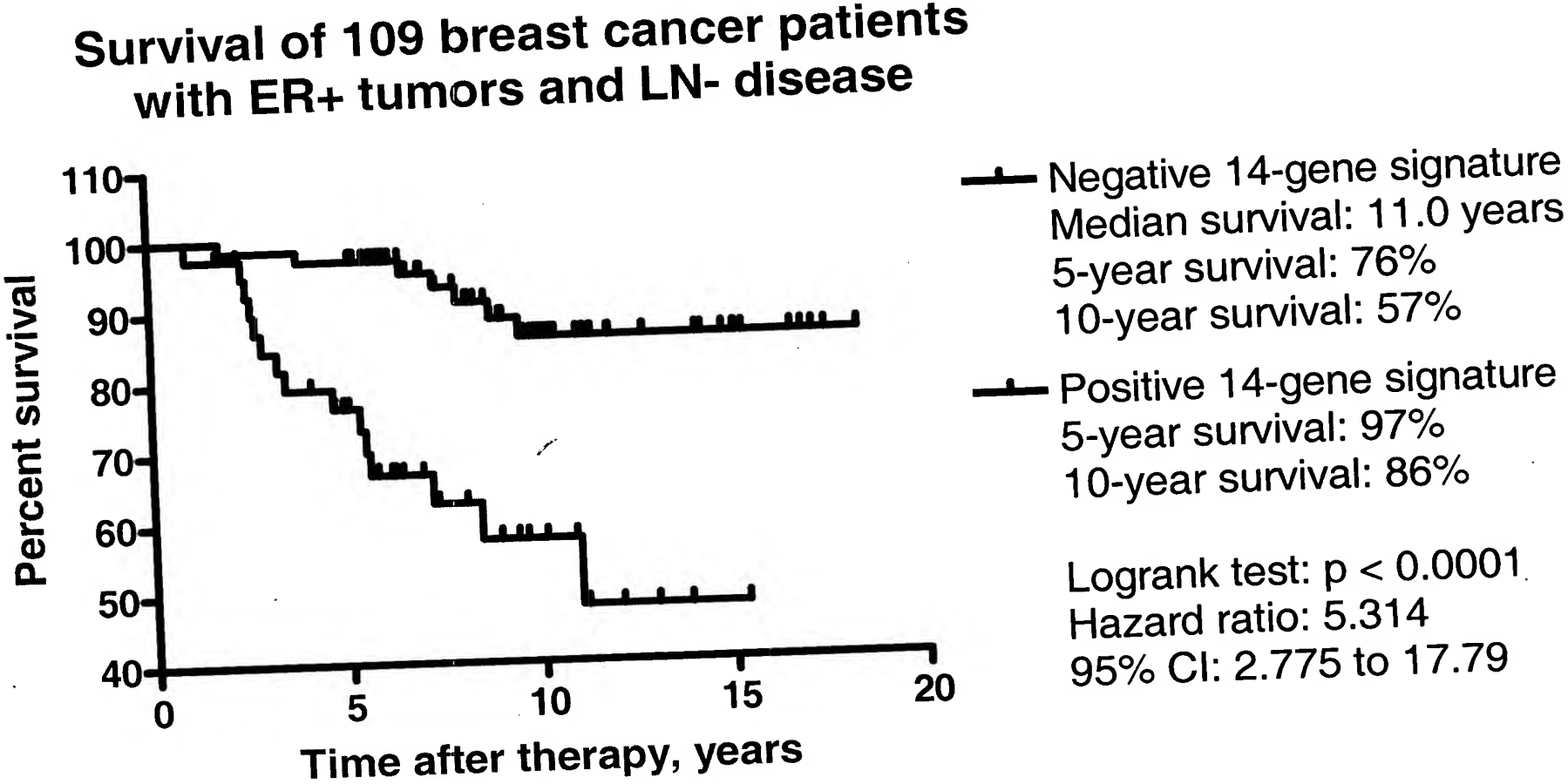


Negative 14-gene signature
Median survival: 7.7 years
5-year survival: 64%
10-year survival: 46%

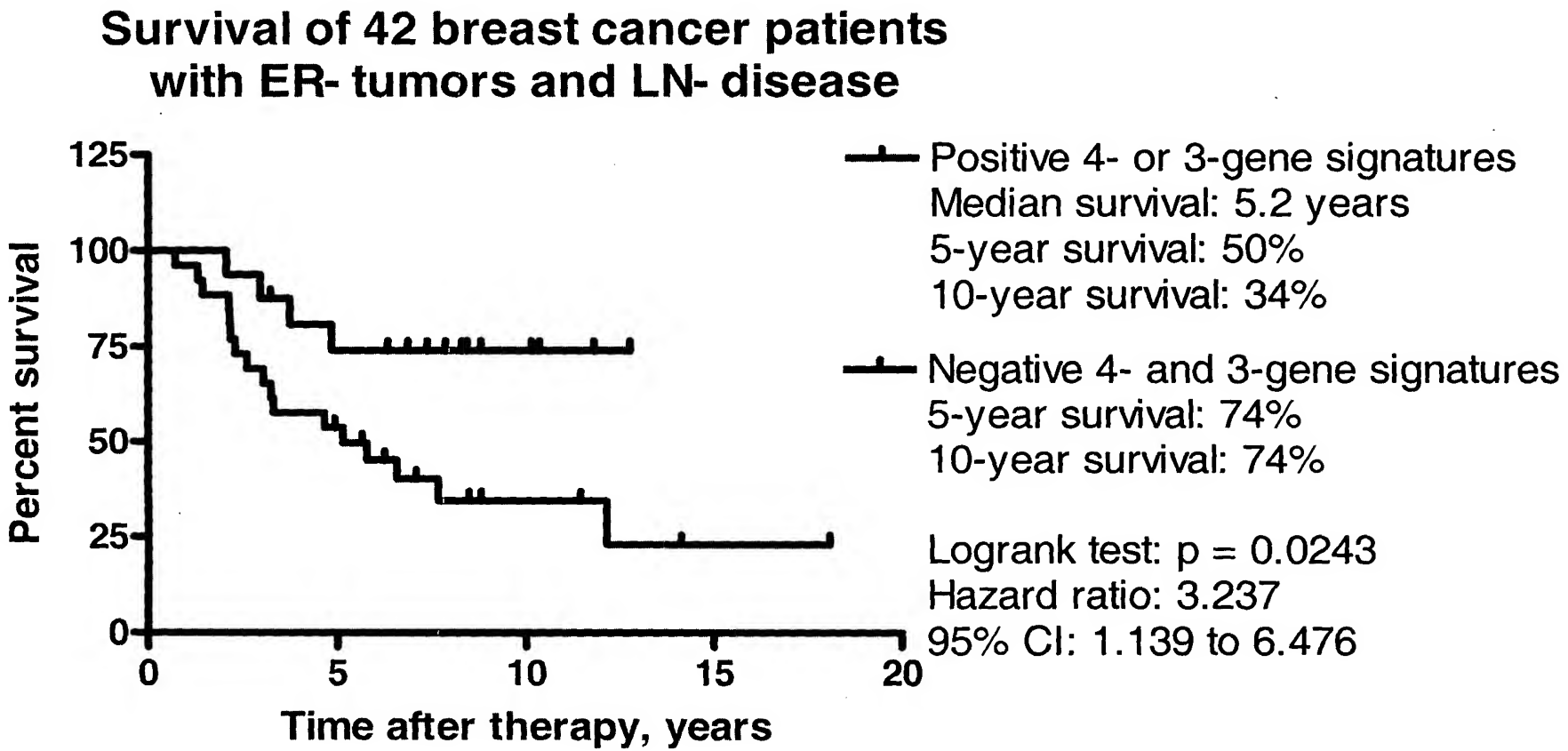
Positive 14-gene signature
5-year survival: 92%
10-year survival: 82%

Logrank test: $p < 0.0001$
Hazard ratio: 5.067
95% CI: 3.174 to 11.57

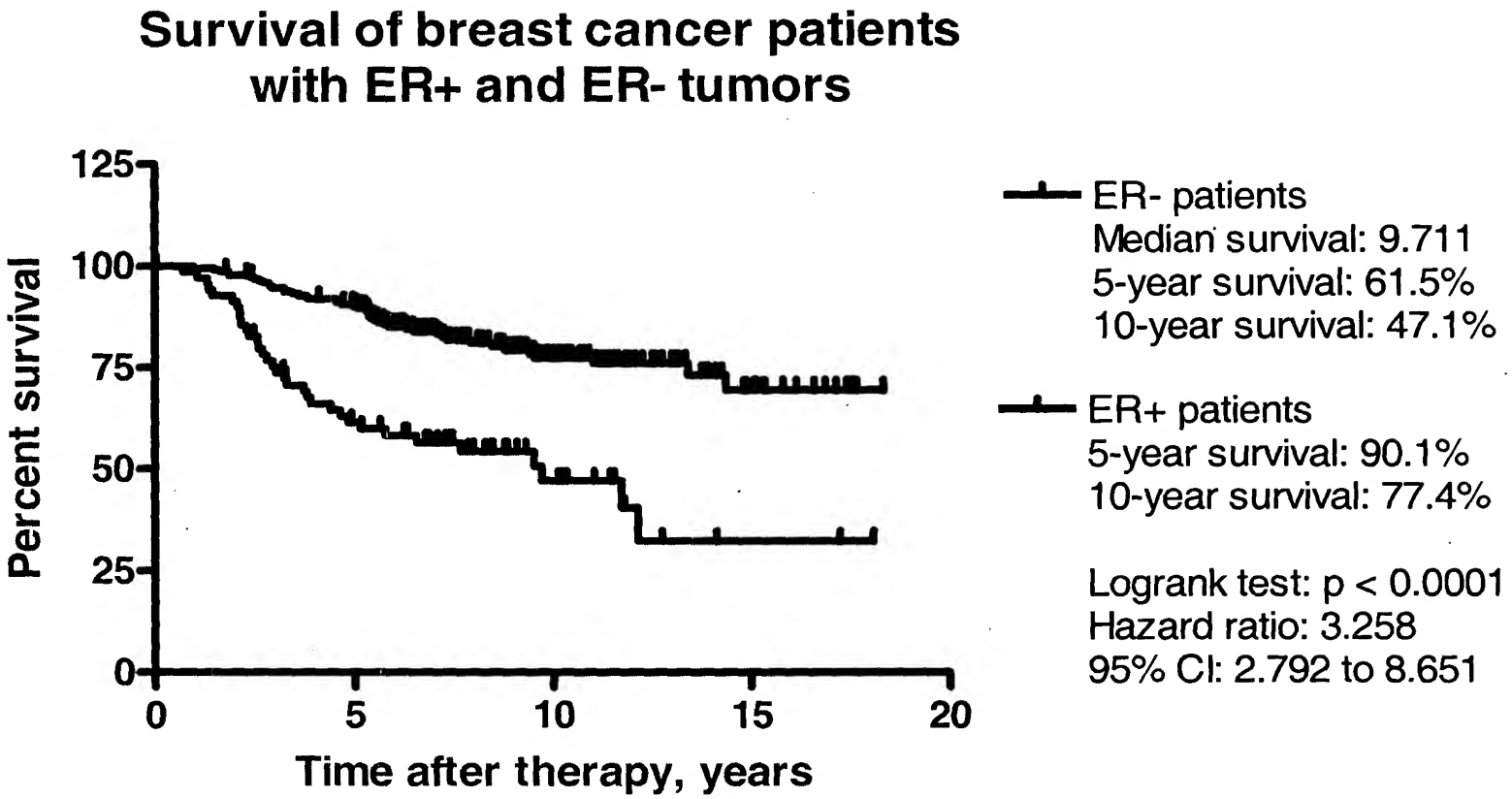
63B


Survival of 109 breast cancer patients
with ER+ tumors and LN- disease
Percent survival
110
100
90
80
70
60
50
40
0
5
10
15
20
Time after therapy, years
Negative 14-gene signature
Median survival: 11.0 years
5-year survival: 76%
10-year survival: 57%
Positive 14-gene signature
5-year survival: 97%
10-year survival: 86%
Logrank test: p < 0.0001
Hazard ratio: 5.314
95% CI: 2.775 to 17.79

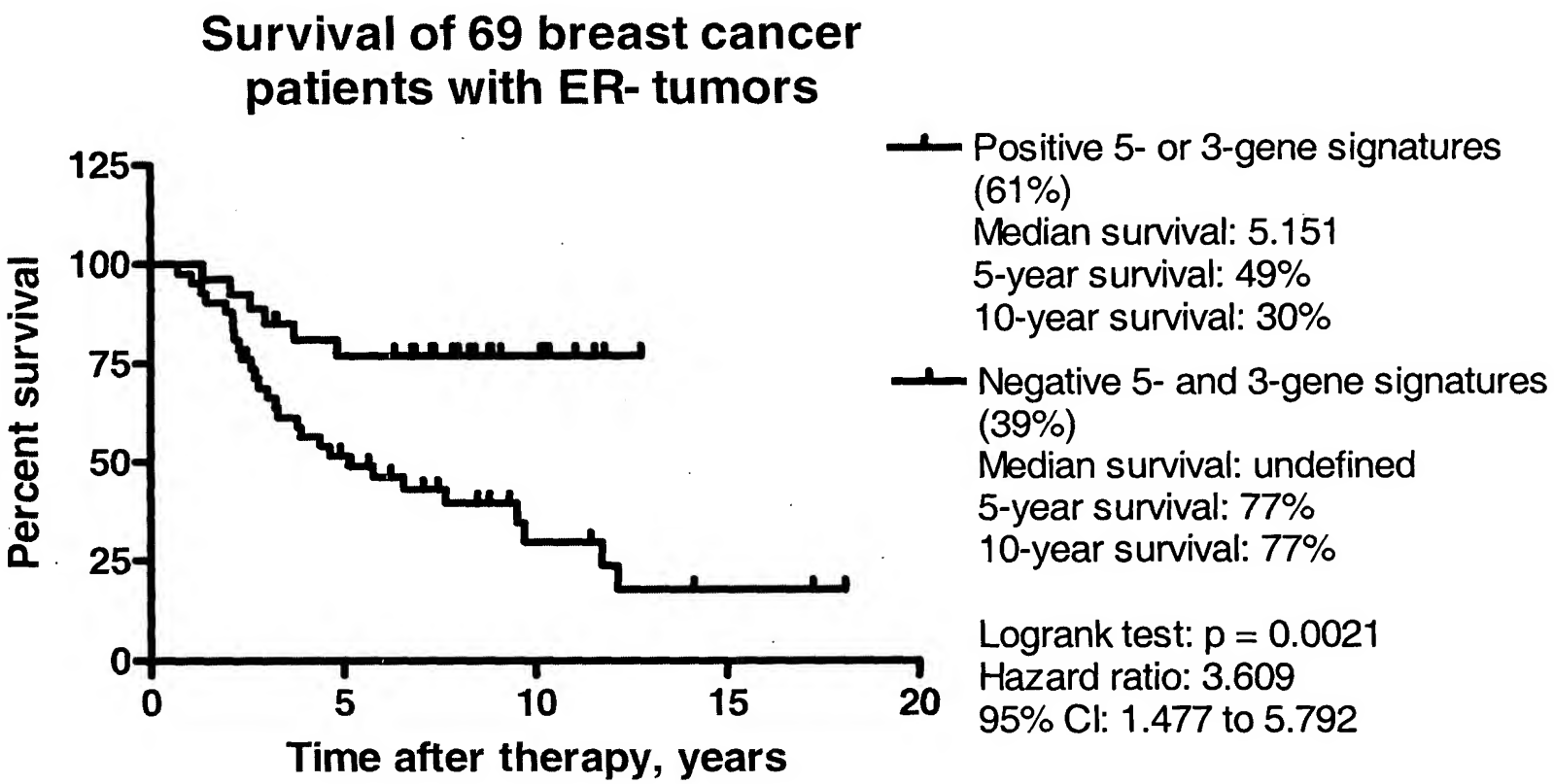
63C


Survival of 42 breast cancer patients
with ER- tumors and LN- disease
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
Positive 4- or 3-gene signatures
Median survival: 5.2 years
5-year survival: 50%
10-year survival: 34%
Negative 4- and 3-gene signatures
5-year survival: 74%
10-year survival: 74%
Logrank test: p = 0.0243
Hazard ratio: 3.237
95% CI: 1.139 to 6.476

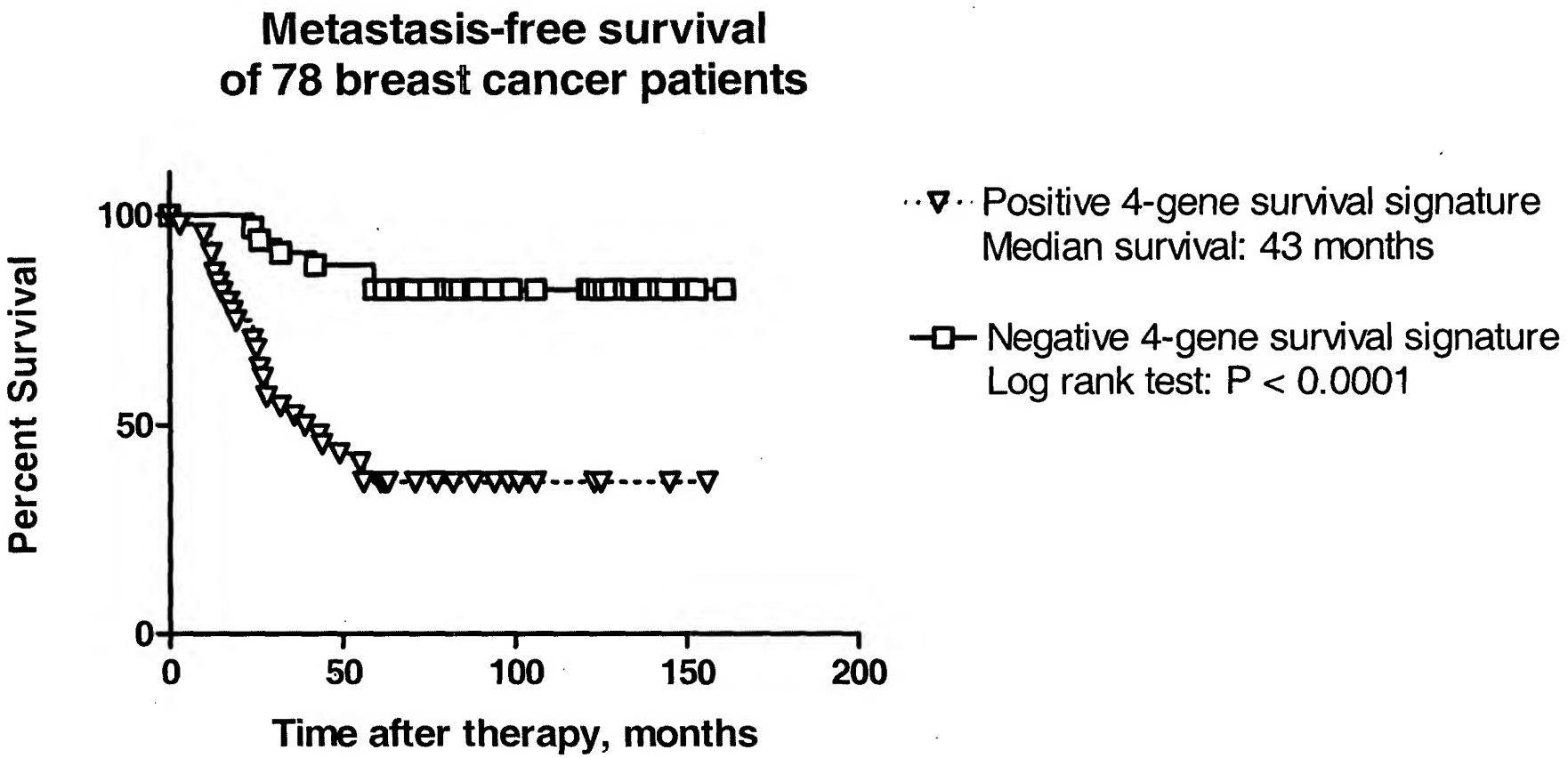
64A


Survival of breast cancer patients
with ER+ and ER- tumors
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
ER- patients
Median survival: 9.711
5-year survival: 61.5%
10-year survival: 47.1%
ER+ patients
5-year survival: 90.1%
10-year survival: 77.4%
Logrank test: p < 0.0001
Hazard ratio: 3.258
95% CI: 2.792 to 8.651

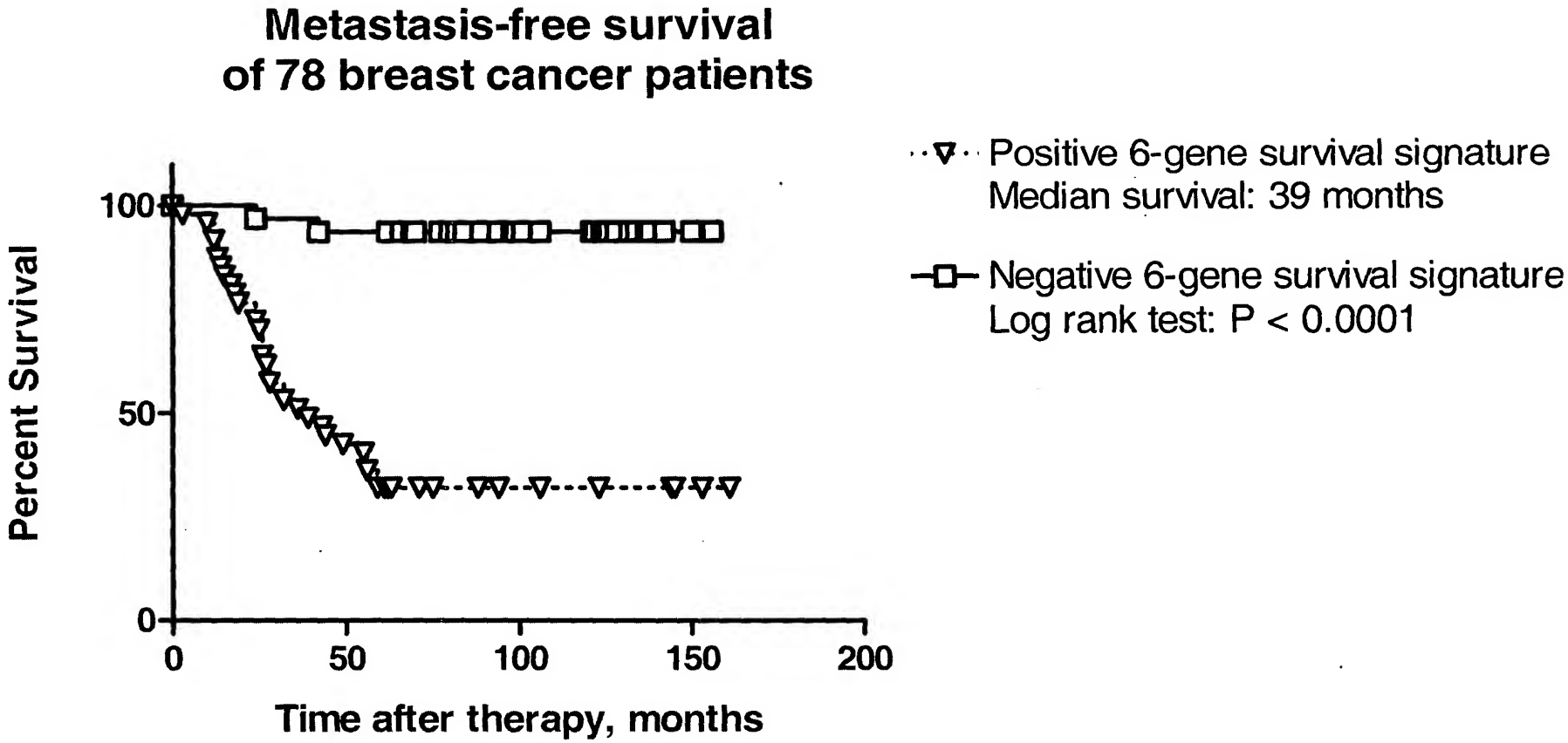
64B


Survival of 69 breast cancer patients with ER- tumors
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
Positive 5- or 3-gene signatures (61%)
Median survival: 5.151
5-year survival: 49%
10-year survival: 30%
Negative 5- and 3-gene signatures (39%)
Median survival: undefined
5-year survival: 77%
10-year survival: 77%
Logrank test: p = 0.0021
Hazard ratio: 3.609
95% CI: 1.477 to 5.792

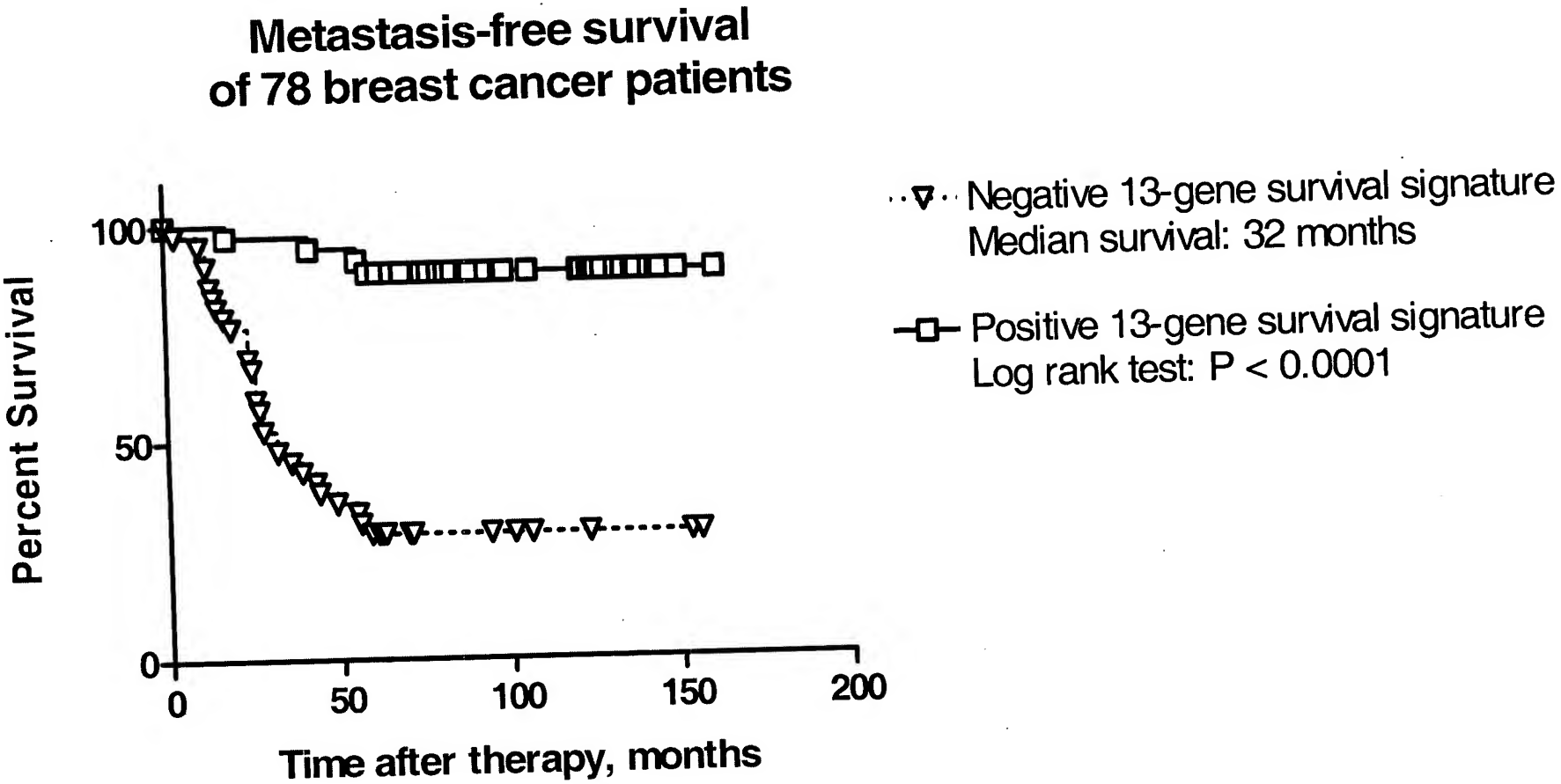
65A


Metastasis-free survival
of 78 breast cancer patients
Percent Survival
100
50
0
0
50
100
150
200
Time after therapy, months
Positive 4-gene survival signature
Median survival: 43 months
Negative 4-gene survival signature
Log rank test: P < 0.0001

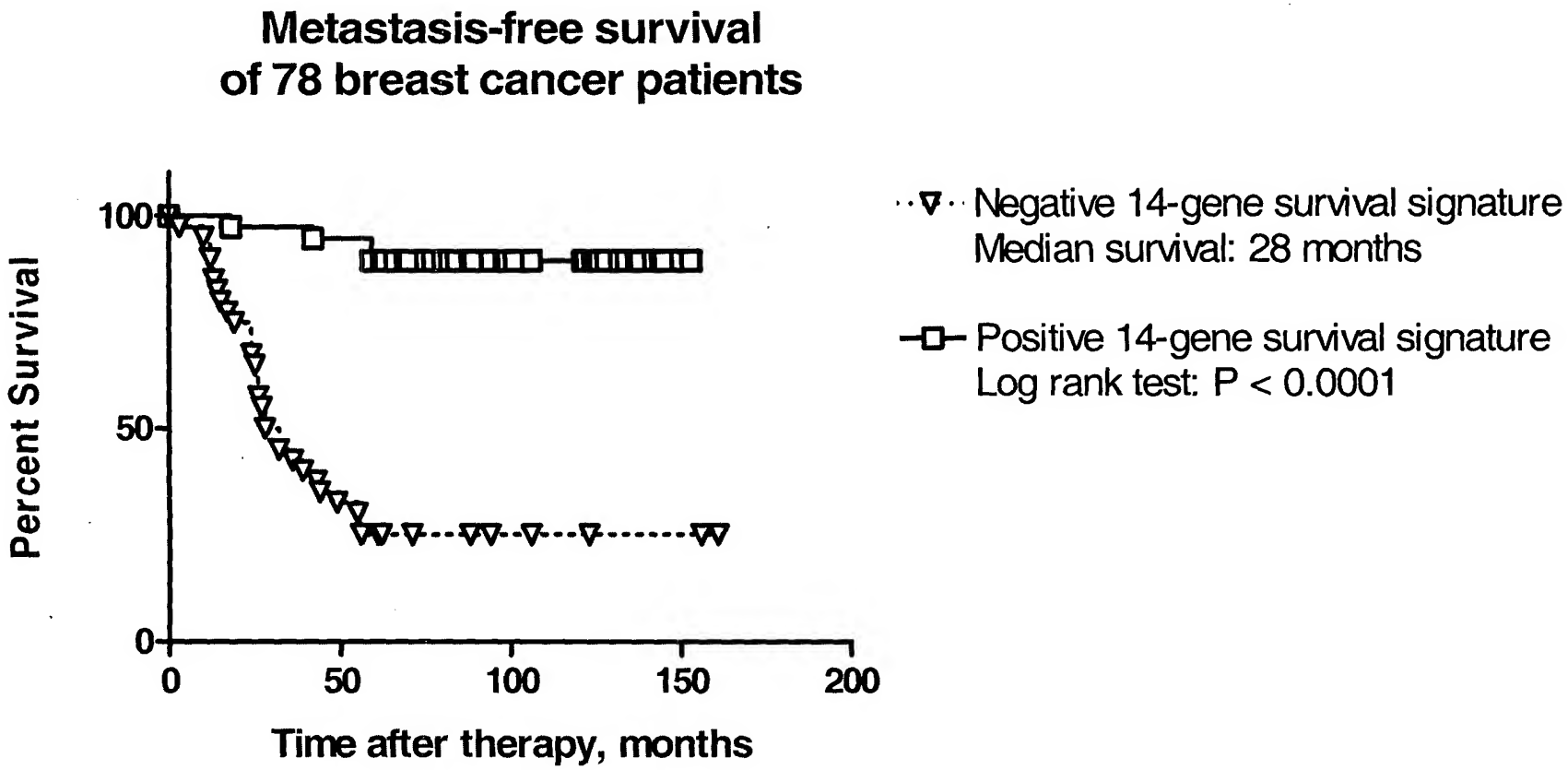
65B


Metastasis-free survival
of 78 breast cancer patients
Percent Survival
100
50
0
0
50
100
150
200
Time after therapy, months
Positive 6-gene survival signature
Median survival: 39 months
Negative 6-gene survival signature
Log rank test: P < 0.0001

65C

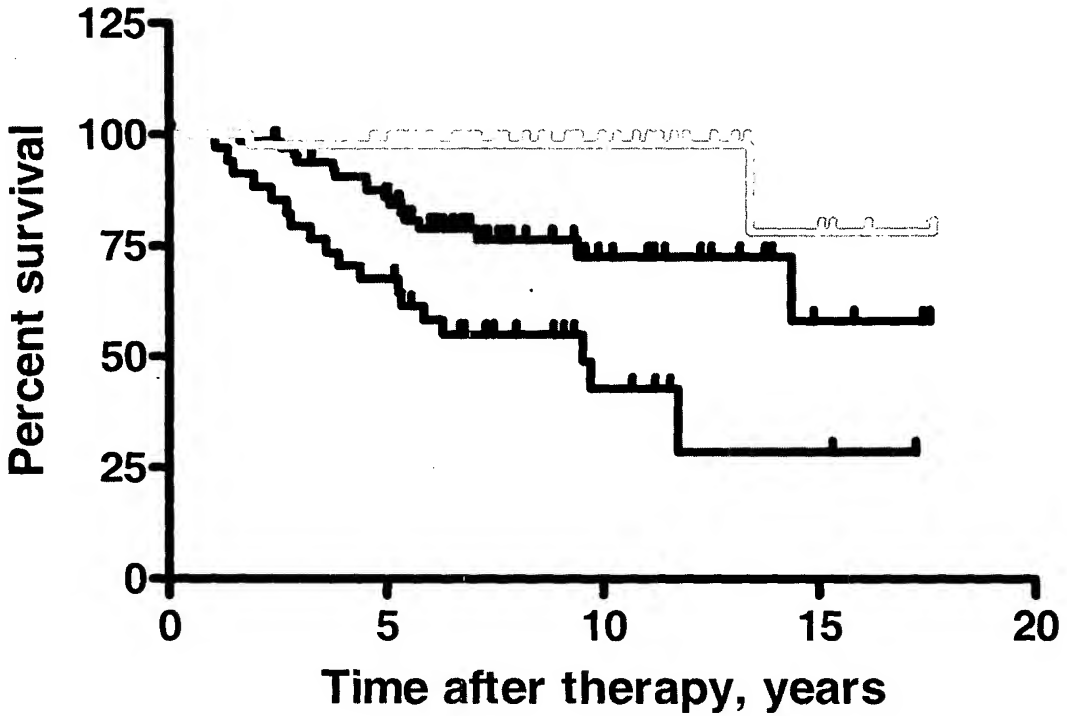

Metastasis-free survival
of 78 breast cancer patients
Percent Survival
100
50
0
0
50
100
150
200
Time after therapy, months
Negative 13-gene survival signature
Median survival: 32 months
Positive 13-gene survival signature
Log rank test: P < 0.0001

65D


Metastasis-free survival
of 78 breast cancer patients
Percent Survival
100
50
0
0
50
100
150
200
Time after therapy, months
Negative 14-gene survival signature
Median survival: 28 months
Positive 14-gene survival signature
Log rank test: P < 0.0001

66A

Survival of 144 breast cancer patients with LN+ disease classified into sub-groups using the 14-gene survival predictor



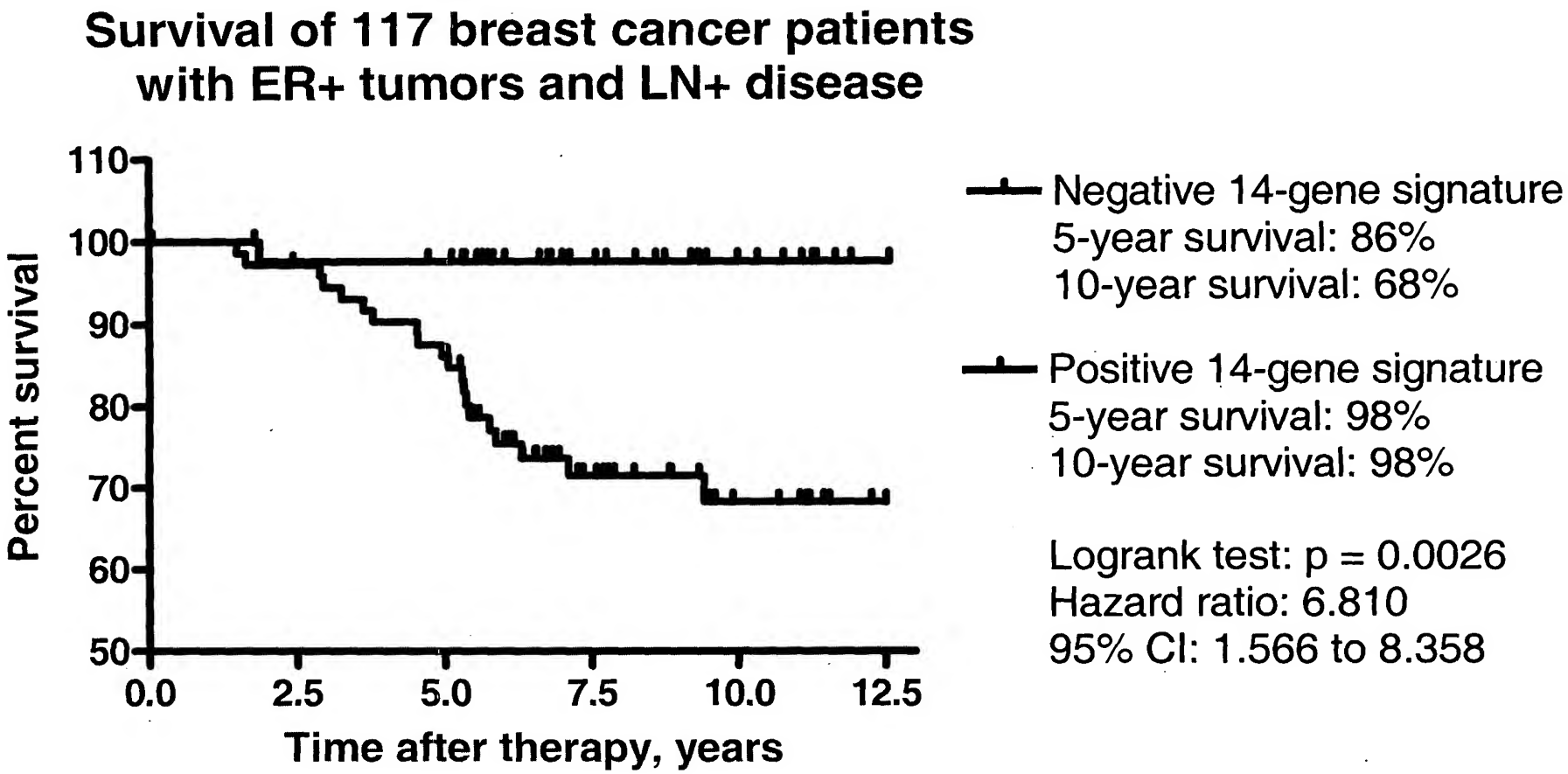
Poor prognosis
Median survival: 9.5 years
5-year survival: 68%
10-year survival: 43%

Intermediate prognosis
5-year survival: 86%
10-year survival: 73%

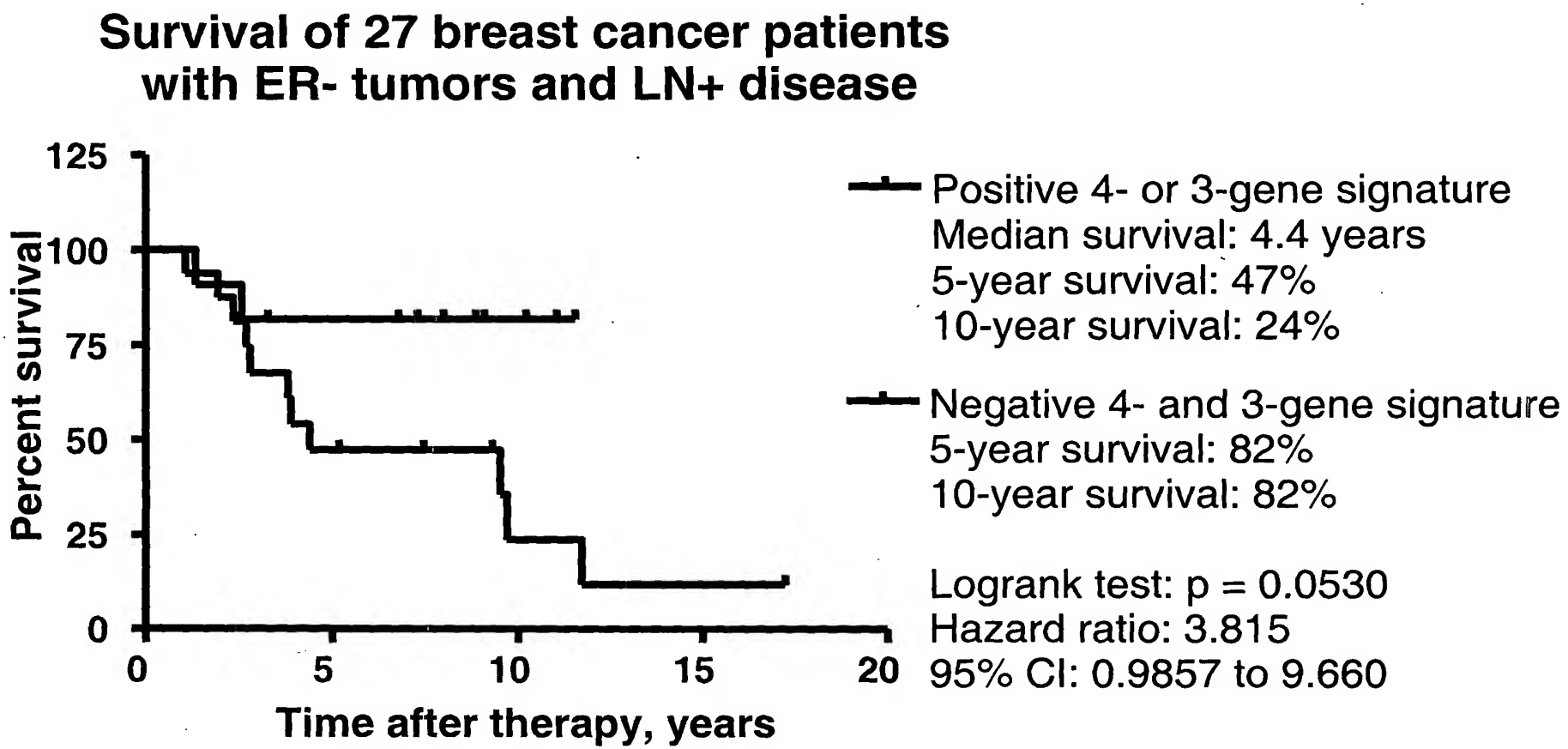
Good prognosis
5-year survival: 98%
10-year survival: 98%

Logrank test: $p < 0.0001$

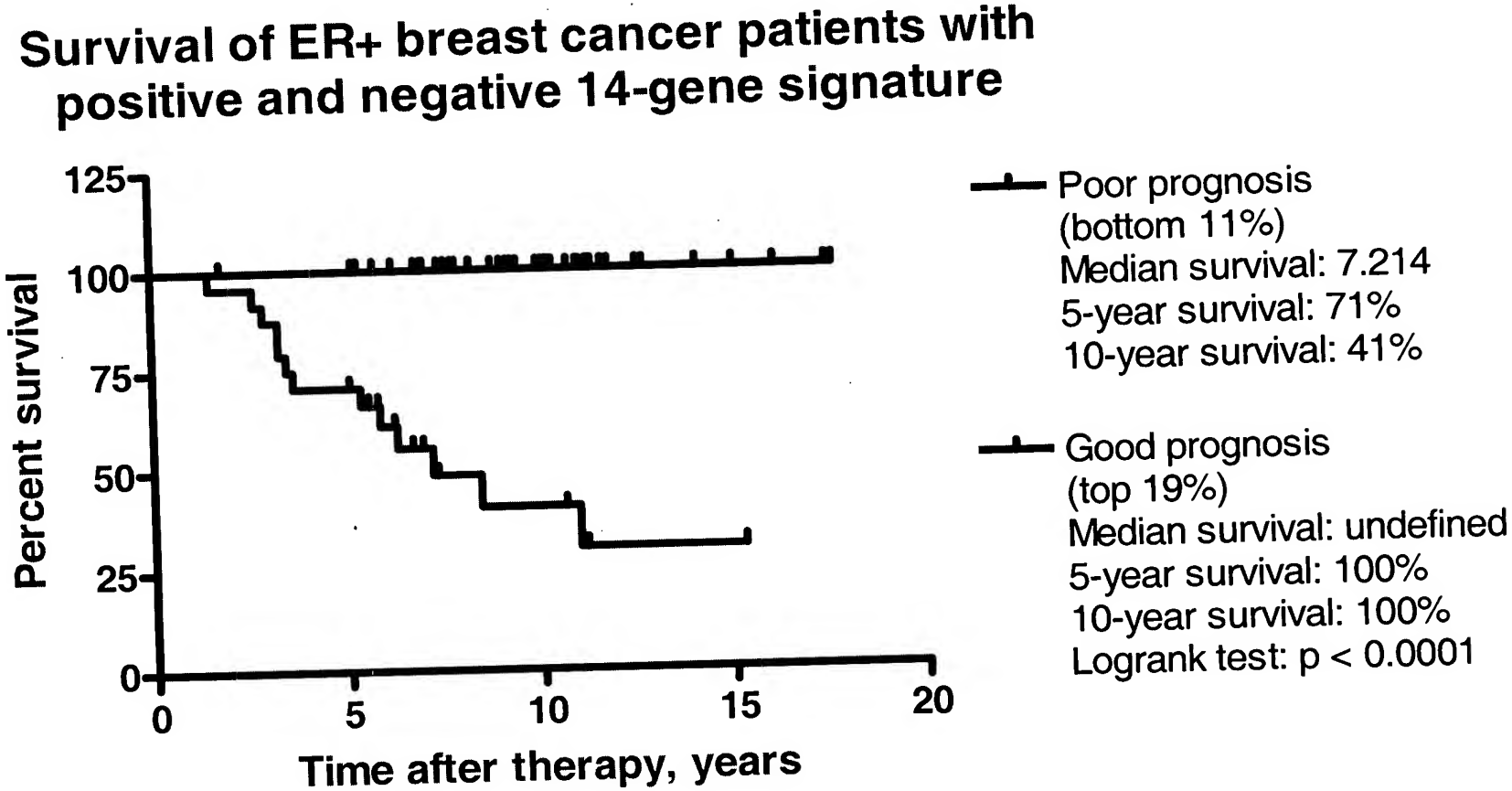
66B


Survival of 117 breast cancer patients
with ER+ tumors and LN+ disease
Percent survival
110
100
90
80
70
60
50
0.0
2.5
5.0
7.5
10.0
12.5
Time after therapy, years
Negative 14-gene signature
5-year survival: 86%
10-year survival: 68%
Positive 14-gene signature
5-year survival: 98%
10-year survival: 98%
Logrank test: p = 0.0026
Hazard ratio: 6.810
95% CI: 1.566 to 8.358

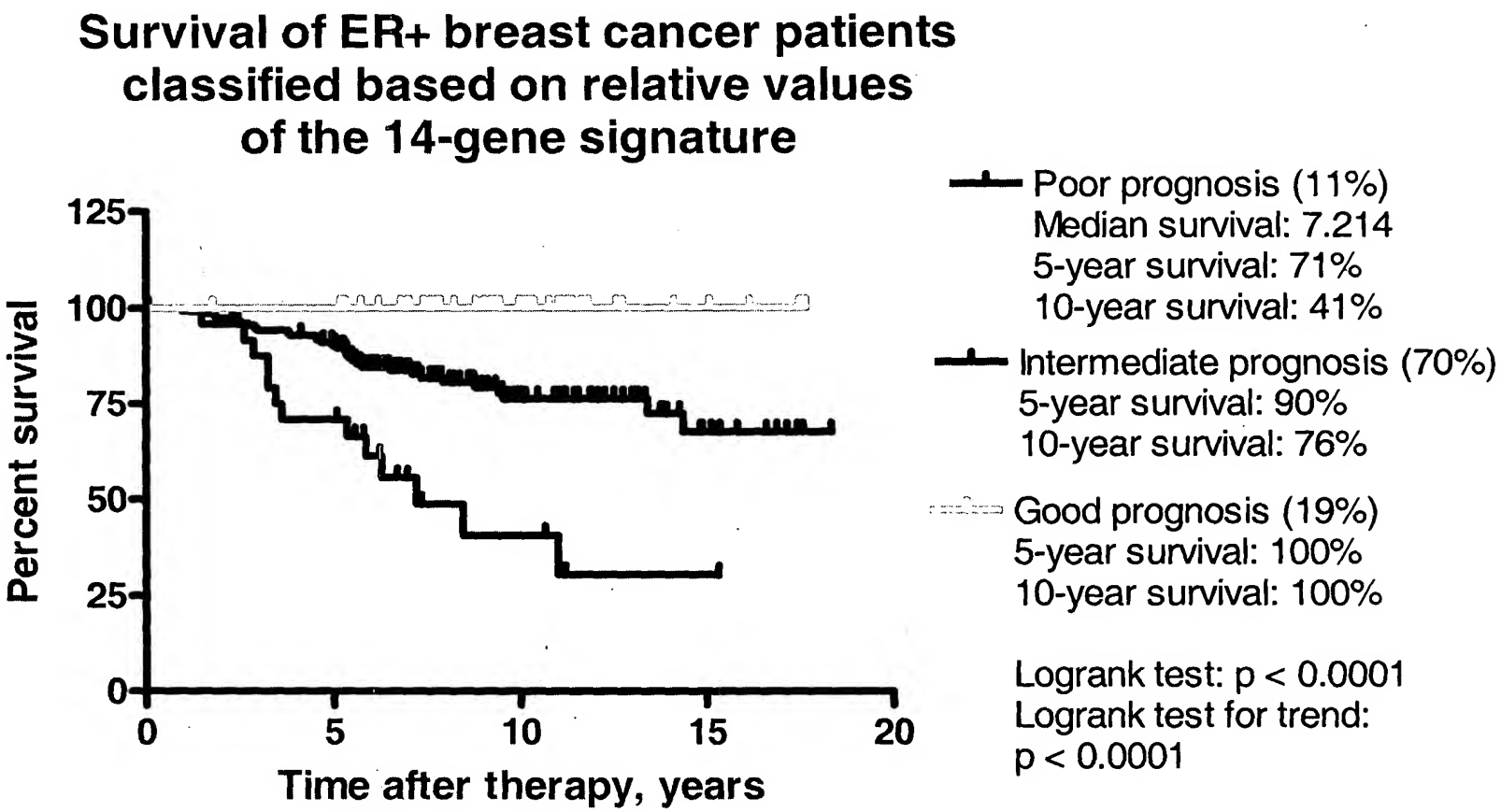
66C


Survival of 27 breast cancer patients
with ER- tumors and LN+ disease
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
Positive 4- or 3-gene signature
Median survival: 4.4 years
5-year survival: 47%
10-year survival: 24%
Negative 4- and 3-gene signature
5-year survival: 82%
10-year survival: 82%
Logrank test: p = 0.0530
Hazard ratio: 3.815
95% CI: 0.9857 to 9.660

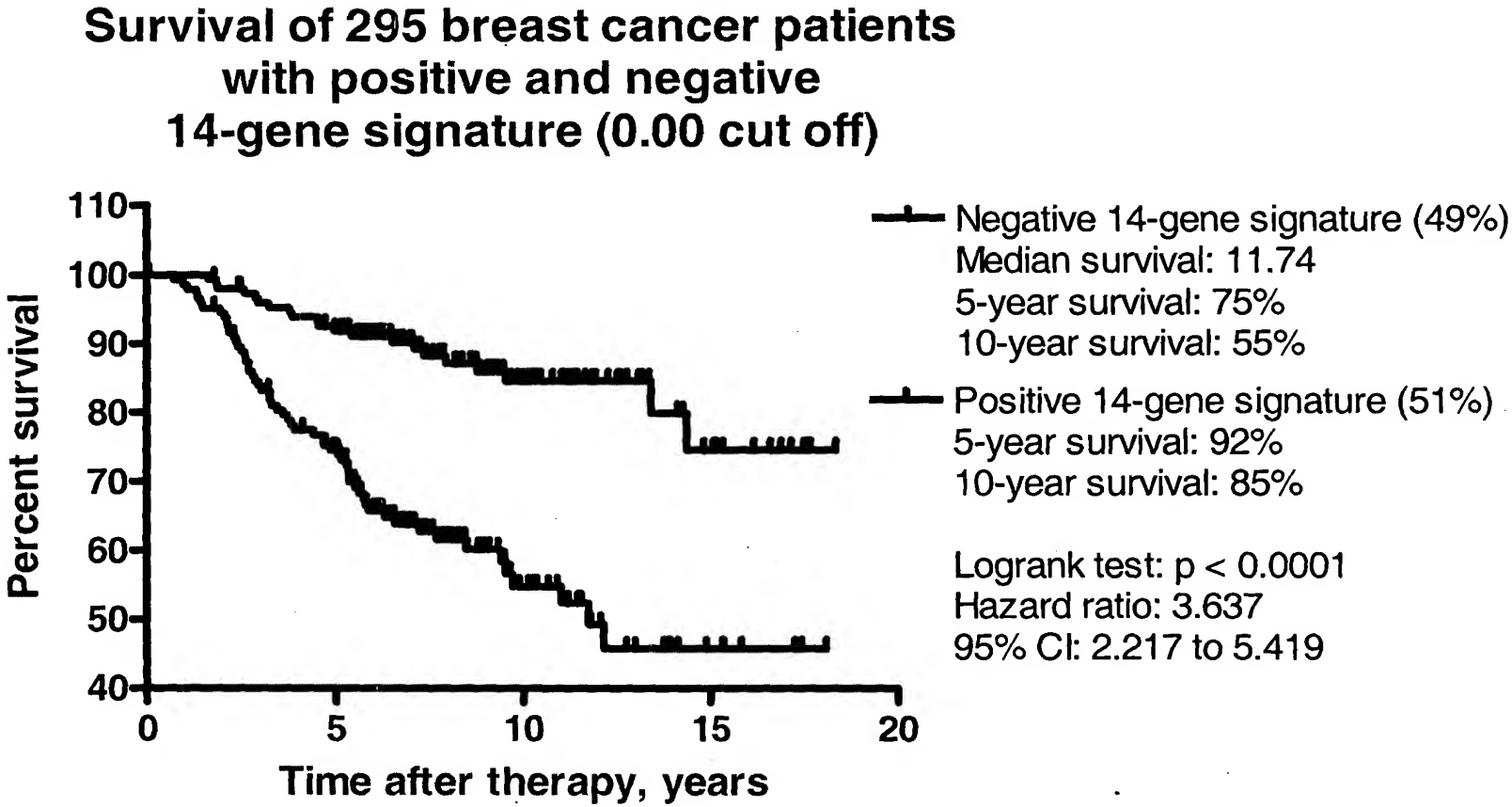
67A


Survival of ER+ breast cancer patients with positive and negative 14-gene signature
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
Poor prognosis
(bottom 11%)
Median survival: 7.214
5-year survival: 71%
10-year survival: 41%
Good prognosis
(top 19%)
Median survival: undefined
5-year survival: 100%
10-year survival: 100%
Logrank test: p < 0.0001

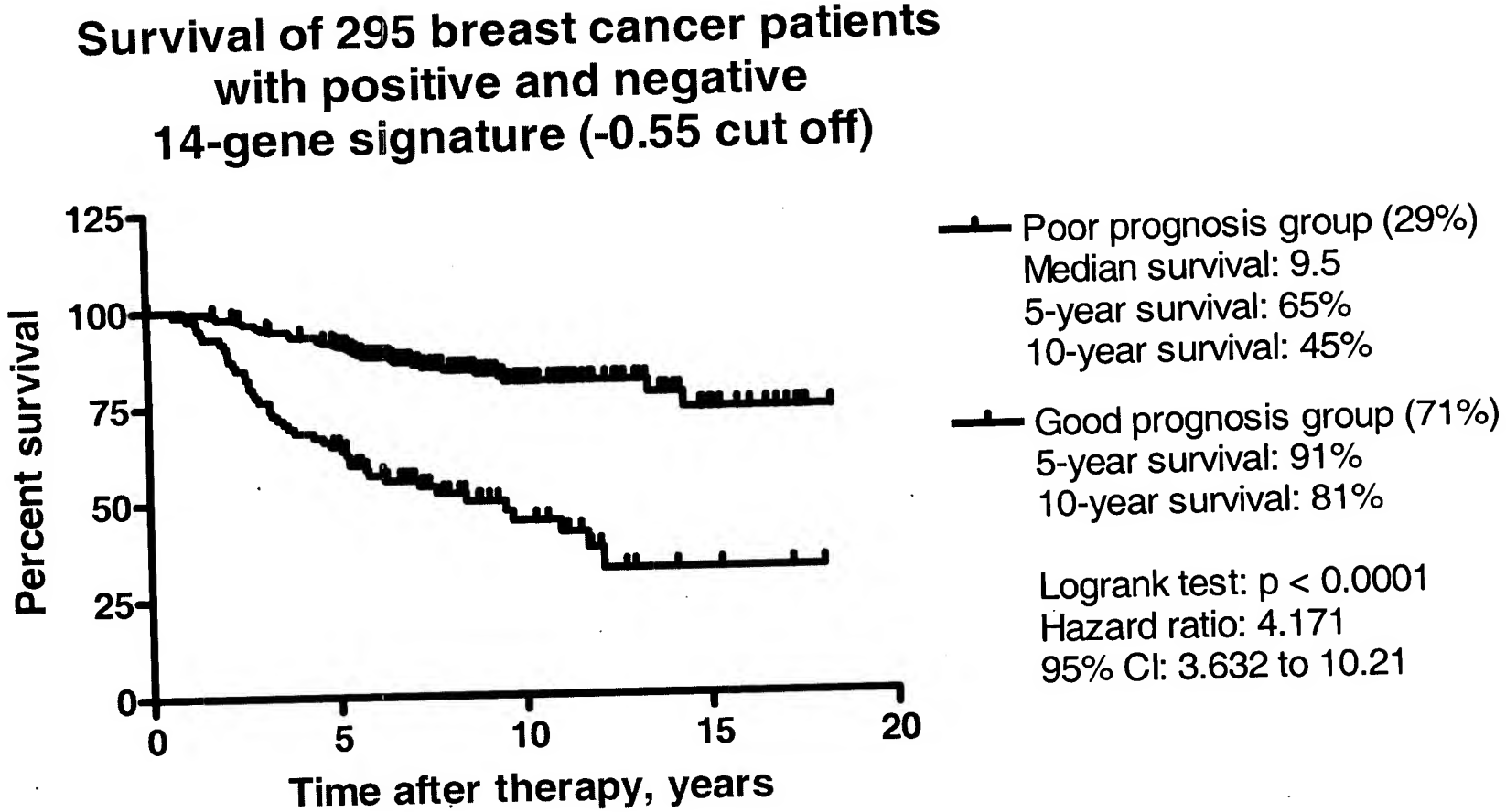
67B


Survival of ER+ breast cancer patients classified based on relative values of the 14-gene signature
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
Poor prognosis (11%)
Median survival: 7.214
5-year survival: 71%
10-year survival: 41%
Intermediate prognosis (70%)
5-year survival: 90%
10-year survival: 76%
Good prognosis (19%)
5-year survival: 100%
10-year survival: 100%
Logrank test: p < 0.0001
Logrank test for trend:
p < 0.0001

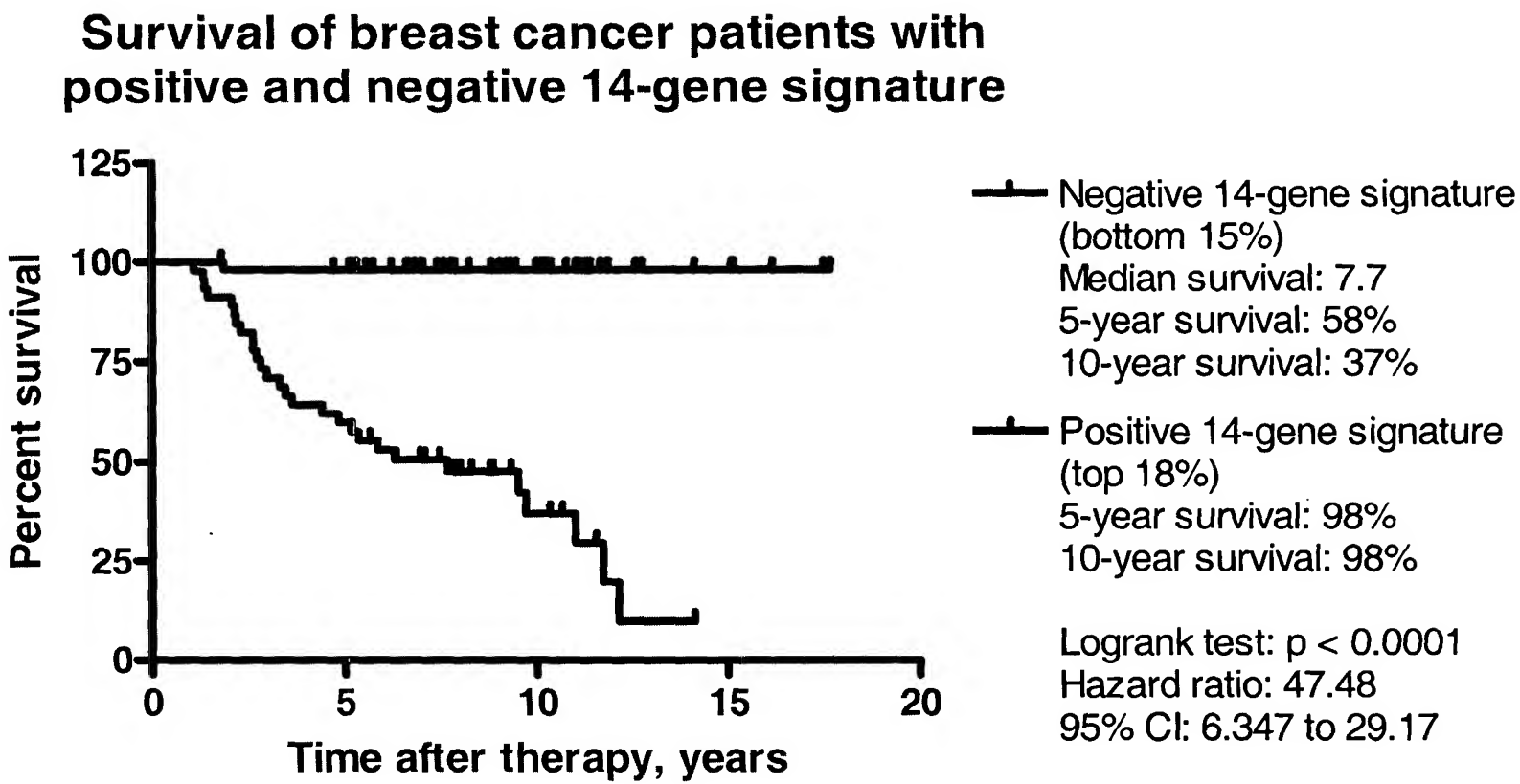
68A


Survival of 295 breast cancer patients
with positive and negative
14-gene signature (0.00 cut off)
Percent survival
110
100
90
80
70
60
50
40
0
5
10
15
20
Time after therapy, years
Negative 14-gene signature (49%)
Median survival: 11.74
5-year survival: 75%
10-year survival: 55%
Positive 14-gene signature (51%)
5-year survival: 92%
10-year survival: 85%
Logrank test: p < 0.0001
Hazard ratio: 3.637
95% CI: 2.217 to 5.419

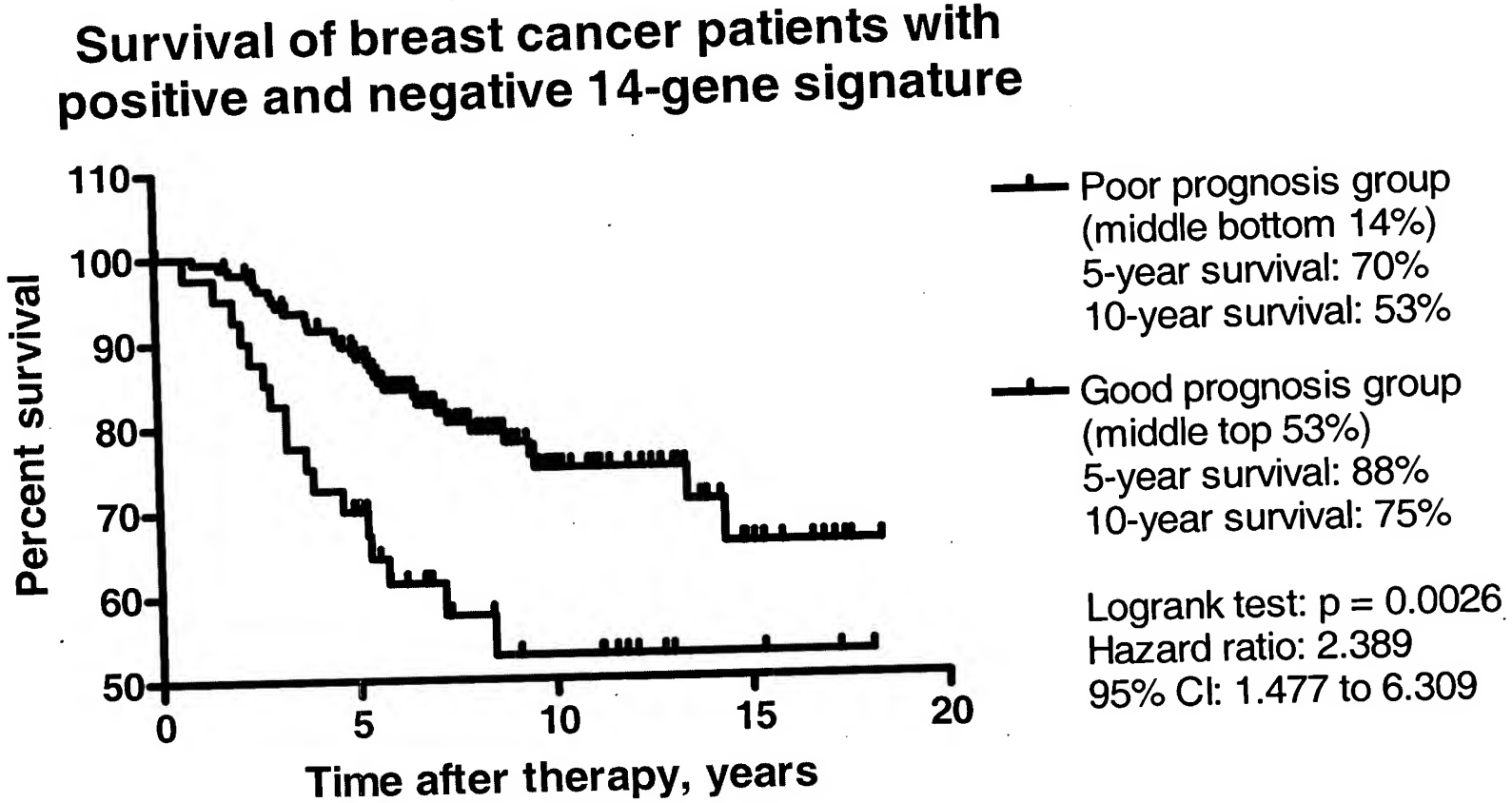
68B


Survival of 295 breast cancer patients
with positive and negative
14-gene signature (-0.55 cut off)
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
Poor prognosis group (29%)
Median survival: 9.5
5-year survival: 65%
10-year survival: 45%
Good prognosis group (71%)
5-year survival: 91%
10-year survival: 81%
Logrank test: p < 0.0001
Hazard ratio: 4.171
95% CI: 3.632 to 10.21

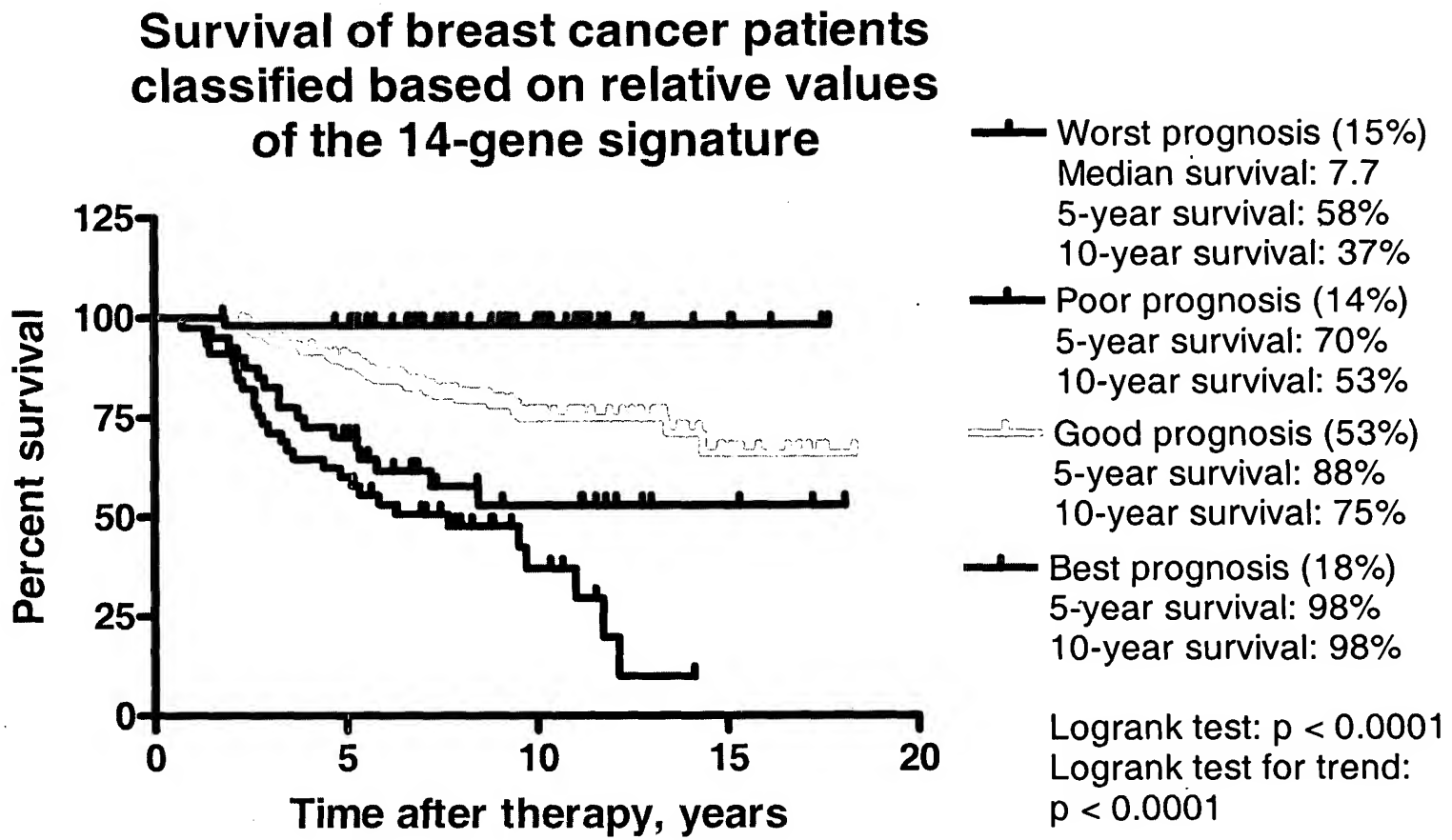
68C


Survival of breast cancer patients with positive and negative 14-gene signature
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
Negative 14-gene signature (bottom 15%)
Median survival: 7.7
5-year survival: 58%
10-year survival: 37%
Positive 14-gene signature (top 18%)
5-year survival: 98%
10-year survival: 98%
Logrank test: p < 0.0001
Hazard ratio: 47.48
95% CI: 6.347 to 29.17

68D


Survival of breast cancer patients with positive and negative 14-gene signature
Percent survival
110
100
90
80
70
60
50
0
5
10
15
20
Time after therapy, years
Poor prognosis group
(middle bottom 14%)
5-year survival: 70%
10-year survival: 53%
Good prognosis group
(middle top 53%)
5-year survival: 88%
10-year survival: 75%
Logrank test: p = 0.0026
Hazard ratio: 2.389
95% CI: 1.477 to 6.309

68E


Survival of breast cancer patients classified based on relative values of the 14-gene signature
Percent survival
125
100
75
50
25
0
0
5
10
15
20
Time after therapy, years
Worst prognosis (15%)
Median survival: 7.7
5-year survival: 58%
10-year survival: 37%
Poor prognosis (14%)
5-year survival: 70%
10-year survival: 53%
Good prognosis (53%)
5-year survival: 88%
10-year survival: 75%
Best prognosis (18%)
5-year survival: 98%
10-year survival: 98%
Logrank test: p < 0.0001
Logrank test for trend:
p < 0.0001